

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:28:25 ; Search time 225 Seconds

(without alignments)
7931.875 Million cell updates/sec

Title: US-10-698-689-85

Perfect score: 1004

Sequence: 1 gctcgtcgggcgcagtc.....ccagtcagtcgacgccttc 1004

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database : Issued Patents NA:*

1: /cgm2_6/ptodata/1/ina/1 COMB.seq:*

2: /cgm2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgm2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgm2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgm2_6/ptodata/1/ina/H COMB.seq:*

6: /cgm2_6/ptodata/1/ina/PCRTUS COMB.seq:*

7: /cgm2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgm2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgm2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	50	5.0	50	3	US-10-131-827-108
2	50	5.0	50	3	US-10-131-827-2096
3	28	2.8	28	2	US-08-859-998-471
C 4	28	2.8	28	2	US-08-859-998-472
5	28	2.8	28	3	US-09-225-928-471
C 6	28	2.8	28	3	US-09-225-928-472
7	28	2.8	28	3	US-09-225-201B-471
C 8	28	2.8	28	3	US-09-225-201B-472
9	25	2.5	25	3	US-09-071-433-88
10	25	2.5	25	3	US-09-344-260A-14
11	25	2.5	25	3	US-09-396-196G-44613
12	25	2.5	25	3	US-09-396-196G-44614
13	25	2.5	25	3	US-09-396-196G-44615
14	25	2.5	25	3	US-09-396-196G-44616
15	25	2.5	25	3	US-09-396-196G-44617
16	25	2.5	25	3	US-09-396-196G-44618
17	25	2.5	25	3	US-09-396-196G-44619
18	25	2.5	25	3	US-09-396-196G-44620
19	25	2.5	25	3	US-09-396-196G-44621
20	25	2.5	25	3	US-09-396-196G-44622
21	25	2.5	25	3	US-09-396-196G-44623
22	25	2.5	25	3	US-09-396-196G-44624
23	25	2.5	25	3	US-09-396-196G-44625
24	25	2.5	25	3	US-09-396-196G-44626

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c 98      19      1.9      40      2      US-08-484-624A-7      Sequence 7, Appli
c 99      19      1.9      40      2      US-08-477-733B-7      Sequence 7, Appli
c 100     19      1.9      40      3      US-09-088-913A-7      Sequence 7, Appli
c 101     19      1.9      40      3      US-08-769-819-7      Sequence 7, Appli
c 102     19      1.9      40      3      US-08-770-974-7      Sequence 7, Appli
c 103     19      1.9      40      3      US-08-770-981-7      Sequence 7, Appli
c 104     19      1.9      40      3      US-09-399-106-7      Sequence 7, Appli
c 105     19      1.9      47      3      US-09-422-978-2564      Sequence 2564, Ap
c 106     19      1.9      50      3      US-08-985-162-1647      Sequence 1647, Ap
c 107     19      1.9      50      3      US-09-401-063-1647      Sequence 1647, Ap
c 108     18.8    1.9      24      3      US-08-697-610-4        Sequence 4, Appli
c 109     18.8    1.9      24      3      US-08-349-357-4        Sequence 4, Appli
c 110     18.8    1.9      25      3      US-09-396-196G-83409      Sequence 83409, A
c 111     18.8    1.9      41      3      US-08-954-210-68        Sequence 68, Appl
c 112     18.8    1.9      41      3      US-09-431-419A-68        Sequence 68, Appl
c 113     18.8    1.9      46      3      US-10-191-540-98        Sequence 98, Appl
c 114     18.8    1.9      47      3      US-09-641-638-961        Sequence 961, App
c 115     18.8    1.9      47      3      US-09-641-638-1257        Sequence 1257, Ap
c 116     18.8    1.9      47      3      US-09-422-978-213        Sequence 213, App
c 117     18.8    1.9      47      3      US-09-422-978-2304        Sequence 2304, Ap
c 118     18.8    1.9      47      3      US-10-170-097-961        Sequence 961, App
c 119     18.8    1.9      47      3      US-10-170-097-1257        Sequence 1257, Ap
c 120     18.8    1.9      48      2      US-08-487-811A-23        Sequence 23, Appli
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ALIGNMENTS

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RESULT 1
US-10-131-827-108
; Sequence 108, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-108
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Query Match      5.0%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      827      GGTCCACCAGGAGTGGCAAGAGAGTGCATCTCAGTCGAGGAGAC      876
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Db      1      GGTCCACCAGGAGTGGCAAGAGAGTGCATCTCAGTCGAGGAGAC      50
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RESULT 2
US-10-131-827-2096
; Sequence 2096, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
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; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2096
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Query Match      5.0%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      834      CAGGAGGATGGCAAGAGAGTGCATCTCAGTCGAGGAGACAGTGAGG      883
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Db      1      CAGGAGGATGGCAAGAGAGTGCATCTCAGTCGAGGAGACAGTGAGG      50
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RESULT 3
US-08-859-998-471
; Sequence 471, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-471
```

Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL EXPRESSION

NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025

STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>

RECEIVED DATE: 03-Mar-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/859,998
 FILING DATE: 21-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Field, Bret E.

NAME: FIELD, ERL E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 471:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs

LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 471:
US-09-225-928-471

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Qy 198 TGCACAGAGTTCACTGAAACGGGAATGCC 225
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Db 1 TGCACAGAGTTCACTGAAACGGGAATGCC 28

; Sequence 472, Application US/09225928
 ; Patent No. 6352829
 ; GENERAL INFORMATION.

APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: CA
 COUNTRY: US

CITY: MENLO PARK
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

Query Match 2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels

Qy 198 TGCACAGATTCACTGAAACGGAATGCC 225
|||
Db 1 TGCACAGATTCACTGAAACGGAATGCC 28

RESULT 6

US-09-225-928-472/c
; Sequence 472, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION.

APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvilli, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

NUMBER OF SEQUENCES: 1375
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: CA
 COUNTRY: US

CITY: MENLO PARK
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

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; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 472:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 472:
US-09-225-928-472
Query Match          2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 577 CAGGCACAAACAGACTGATGTTGCTG 604
Db 28 CAGGCACAAACAGACTGATGTTGCTG 1

RESULT 7
US-09-225-201B-471
; Sequence 471, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;      Johhadze, George
;      Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;      EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
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;
; INFORMATION FOR SEQ ID NO: 471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 471:
US-09-225-201B-471
Query Match          2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 TGCACAGAGTTCACCTGAAACGGATGCC 225
Db 1 TGCACAGAGTTCACCTGAAACGGATGCC 28

RESULT 8
US-09-225-201B-472/c
; Sequence 472, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;      Johhadze, George
;      Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;      EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 472:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 472:
US-09-225-201B-472
Query Match          2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 577 CAGGCACAAACAAGACTGATGTTGCTG 604
Db 28 CAGGCACAAACAAGACTGATGTTGCTG 1

RESULT 9

US-09-071-433-88
; Sequence 88, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsert, Lex M
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-071-433-88

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAGCGAATTCCT 250
Db 1 TTCCTTGGGTGAAGCGAATTCCT 25

RESULT 10

US-09-344-260A-14
; Sequence 14, Application US/09344260A
; Patent No. 6576752
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Virta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS-3508
; CURRENT APPLICATION NUMBER: US/09/344,260A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576752e1 Sequence
US-09-344-260A-14

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAGCGAATTCCT 250
Db 1 TTCCTTGGGTGAAGCGAATTCCT 25

RESULT 11

US-09-396-196G-44613

; Sequence 44613, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44613

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGGTTGCTGCTCTGCGTCTGCGTGG 72
Db 1 ATGGTTGCTGCTCTGCGTCTGCGTGG 25

RESULT 12

US-09-396-196G-44614
; Sequence 44614, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44614

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CGTCTGCTCTGCGTGGTCTCTCT 78
Db 1 CGTCTGCTCTGCGTGGTCTCTCT 25

RESULT 13

US-09-396-196G-44615
; Sequence 44615, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

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; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44615
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44615

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 TTGTGCCAGCCAGCAGACAGAACTGG 189
Db 1 TTGTGCCAGCCAGCAGACAGAACTGG 25

RESULT 14
US-09-396-196G-44616
; Sequence 44616, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44616

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GACTGCACAGAGTTCACTGAAACGG 219
Db 1 GACTGCACAGAGTTCACTGAAACGG 25

RESULT 15
US-09-396-196G-44617
; Sequence 44617, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44617
```

```
; ORGANISM: mus musculus
US-09-396-196G-44617

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 GAAACGGAATGCCTTCCTTCGGGTG 237
Db 1 GAAACGGAATGCCTTCCTTCGGGTG 25

RESULT 16
US-09-396-196G-44618
; Sequence 44618, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44618

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 GAATGCCTTCCTTCGGGTGAAACGG 243
Db 1 GAATGCCTTCCTTCGGGTGAAACGG 25

RESULT 17
US-09-396-196G-44619
; Sequence 44619, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44619

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 TGCCTTCCTTCGGGTGAAACGGAAT 246
Db 1 TGCCTTCCTTCGGGTGAAACGGAAT 246
```

Db 1 TGCCTTCTTCGGTGGAAGCGAAT 25

RESULT 18

US-09-396-196G-44620
; Sequence 44620, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 60/100,678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44620
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44620

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred.No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 240 AGCGAATTCCTAGACACCTGGGAACA 264

Db 1 AGCGAATTCCTAGACACCTGGGAACA 25

RESULT 19

US-09-396-196G-44621
; Sequence 44621, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 60/100,678
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44621

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred.No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 GAATTCCTAGACACCTGGGAACAGAG 267

Db 1 GAATTCCTAGACACCTGGGAACAGAG 25

RESULT 20

US-09-396-196G-44622
; Sequence 44622, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44622

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred.No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 AGAGAGACACACTGCCACCAGCACA 288

Db 1 AGAGAGACACACTGCCACCAGCACA 25

RESULT 21

US-09-396-196G-44623
; Sequence 44623, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44623
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44623

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred.No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CACTGCCACCAGCACAATACTGCG 297

Db 1 CACTGCCACCAGCACAATACTGCG 25

RESULT 22

US-09-396-196G-44624
; Sequence 44624, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

```
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44624

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      276 TGCCACCAGCACAATACTGCGACC 300
Db      1 TGCCACCAGCACAATACTGCGACC 25

RESULT 23
US-09-396-196G-44625
; Sequence 44625, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44625

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      57 CTGCGCTCTGCAGTCGCTCCTCTGGG 81
Db      1 CTGCGCTCTGCAGTCGCTCCTCTGGG 25

RESULT 24
US-09-396-196G-44626
; Sequence 44626, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44626

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      57 CTGCGCTCTGCAGTCGCTCCTCTGGG 81
Db      1 CTGCGCTCTGCAGTCGCTCCTCTGGG 25

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      60 CCTCTGCAGTCGCTCCTCTGGGGCT 84
Db      1 CCTCTGCAGTCGCTCCTCTGGGGCT 25

RESULT 25
US-09-396-196G-44627
; Sequence 44627, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44627

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      63 CTGCAGTCGCTCCTCTCTGGGGCTGCT 87
Db      1 CTGCAGTCGCTCCTCTCTGGGGCTGCT 25

RESULT 26
US-09-396-196G-44628
; Sequence 44628, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44628

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      87 TTGCTGACCGCTGTCCATCCAGAAC 111
Db      1 TTGCTGACCGCTGTCCATCCAGAAC 25

RESULT 27
```

US-09-396-196G-44629
; Sequence 44629, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44629

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CCCACTGCATGCAGAGAAAACAGT 138
|||||
Db 1 CCCACTGCATGCAGAGAAAACAGT 25

RESULT 28
US-09-396-196G-44630
; Sequence 44630, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44630
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44630

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 TACCTAATAAAGTCAGTCGTGTT 162
|||||
Db 1 TACCTAATAAAGTCAGTCGTGTT 25

RESULT 29
US-09-396-196G-44631
; Sequence 44631, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44631

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AACAGTCAGTCGTCTTTTGCC 171
|||||
Db 1 AACAGTCAGTCGTCTTTTGCC 25

RESULT 30
US-09-396-196G-44632
; Sequence 44632, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44632
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44632

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 TCTTTGTCAGCCAGGACAGAAAC 186
|||||
Db 1 TCTTTGTCAGCCAGGACAGAAAC 25

RESULT 31
US-10-234-764-14
; Sequence 14, Application US/10234764
; Patent No. 6825331
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Vitta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS5089
; CURRENT APPLICATION NUMBER: US/10/234,764
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 09/344,260
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2

```
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-234-764-14

Query Match          2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGCGTGAAGCGCAATTCCT 250
      |||||
Db 1 TTCCTTGGCGTGAAGCGCAATTCCT 25

RESULT 32
US-07-910-222B-5
; Sequence 5, Application US/07910222B
; Patent No. 5397703
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: A Method for Generation of Antibodies to
; TITLE OF INVENTION: Cell Surface Molecules
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Oncology Corporation
; STREET: 1400 53rd Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,222B
; FILING DATE: 19920709
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 2255-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 420-3300
; TELEFAX: (510) 658-5470
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Forward Primer for CD40, MR108
; US-07-910-222B-5

Query Match          2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCCATGTTG 55
      |||||
Db 9 CTGGTCTCACCTCGCCCATGTTG 32

RESULT 34
US-08-070-158-5
; Sequence 5, Application US/08070158
; Patent No. 5677165
; GENERAL INFORMATION:
; APPLICANT: DE BOER, MARK
; APPLICANT: CONROY, LEAH B.
; TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
; TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; US-08-070-158-5

Query Match          2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCCATGTTG 55
      |||||
Db 9 CTGGTCTCACCTCGCCCATGTTG 32

RESULT 33
US-07-910-222B-5
; Sequence 5, Application US/07910222B
; Patent No. 5397703
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: A Method for Generation of Antibodies to
; TITLE OF INVENTION: Cell Surface Molecules
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Oncology Corporation
; STREET: 1400 53rd Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,222B
; FILING DATE: 19920709
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 2255-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 420-3300
; TELEFAX: (510) 658-5470
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Forward Primer for CD40, MR108
; US-07-910-222B-5

Query Match          2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCCATGTTG 55
      |||||
Db 9 CTGGTCTCACCTCGCCCATGTTG 32

RESULT 33
US-07-910-222B-5
; Sequence 5, Application US/07910222B
; Patent No. 5397703
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: A Method for Generation of Antibodies to
; TITLE OF INVENTION: Cell Surface Molecules
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Oncology Corporation
; STREET: 1400 53rd Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,222B
; FILING DATE: 19920709
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 2255-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 420-3300
; TELEFAX: (510) 658-5470
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Forward Primer for Soluble CD40,
; INDIVIDUAL ISOLATE: MR108
; US-07-910-222B-7

Query Match          2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCCATGTTG 55
      |||||
Db 9 CTGGTCTCACCTCGCCCATGTTG 32

RESULT 34
US-08-070-158-5
; Sequence 5, Application US/08070158
; Patent No. 5677165
; GENERAL INFORMATION:
; APPLICANT: DE BOER, MARK
; APPLICANT: CONROY, LEAH B.
; TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
; TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; US-08-070-158-5
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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/070,158
;; FILING DATE: 28-MAY-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McGarrigle, Philip L.
;; REGISTRATION NUMBER: 31,395
;; REFERENCE/DOCKET NUMBER: 0925.003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 601-2718
;; TELEFAX: (510) 655-3542
;; TELEX: n/a
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-070-158-5

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
DB 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 35
US-08-200-716-5
; Sequence 5, Application US/08200716
; Patent No. 5747034
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods and Materials for Induction
; TITLE OF INVENTION: of T Cell Anergy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)
US-08-200-716-5

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
DB 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 36
US-08-200-716-7
; Sequence 7, Application US/08200716
; Patent No. 5747034
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods and Materials for Induction
; TITLE OF INVENTION: of T Cell Anergy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-716-7

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
DB 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 37
US-08-015-147-5
; Sequence 5, Application US/08015147
; Patent No. 5869050
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods of Blocking T-Cell
; TITLE OF INVENTION: Activation Using
; TITLE OF INVENTION: Anti-B7 Monoclonal Antibodies

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,147
FILING DATE: 02-FEB-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,222
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 31411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Forward Primer for CD40, MR108
US-08-015-147-5

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTGCCCATGGTTGC 55
Db 9 CTGGTCTCACCTGCCCATGGTTGC 32

RESULT 38
US-08-015-147-7
Sequence 7, Application US/08015147
Patent No. 5869050
GENERAL INFORMATION:
APPLICANT: de Boer, Mark
APPLICANT: Conroy, Leah B.
TITLE OF INVENTION: Methods of Blocking T-Cell
TITLE OF INVENTION: Activation Using
TITLE OF INVENTION: Anti-B7 Monoclonal Antibodies
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,147
FILING DATE: 02-FEB-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,222
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 31411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Forward Primer for Soluble
INDIVIDUAL ISOLATE: CD40, MR108
US-08-015-147-7

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTGCCCATGGTTGC 55
Db 9 CTGGTCTCACCTGCCCATGGTTGC 32

RESULT 39
US-08-469-015-5
Sequence 5, Application US/08469015
Patent No. 6004552
GENERAL INFORMATION:
APPLICANT: DE BOER, MARK
APPLICANT: CONROY, LEAH B.
TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,015
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/070,158
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle, Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0925.003

TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-015-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTCG 32

RESULT 40

US-08-463-893-5

Sequence 5, Application US/08463893

Patent No. 6056959

GENERAL INFORMATION:

APPLICANT: DE BOER, MARK

APPLICANT: CONROY, LEAH B.

TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION

USING ANTI-CD40 MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: 4560 Horton Street, R-440

CITY: Emeryville

STATE: California

COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,893

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/070,158

FILING DATE: 28-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: McGarrigle, Philip L.

REGISTRATION NUMBER: 31,395

REFERENCE/DOCKET NUMBER: 0925.003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2718

TELEFAX: (510) 655-3542

TELEX: n/a

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-463-893-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTCG 55

Db 9 CTGGTCTCACCTCGCCATGGTTCG 32

RESULT 41

US-09-504-505-5

Sequence 5, Application US/09504505

Patent No. 6315998

GENERAL INFORMATION:

APPLICANT: DE BOER, MARK

APPLICANT: CONROY, LEAH B.

TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION

USING ANTI-CD40 MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: 4560 Horton Street, R-440

CITY: Emeryville

STATE: California

COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/504,505

FILING DATE: 15-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/463,893

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US/08/070,158

FILING DATE: 28-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: McGarrigle, Philip L.

REGISTRATION NUMBER: 31,395

REFERENCE/DOCKET NUMBER: 0925.003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2718

TELEFAX: (510) 655-3542

TELEX: n/a

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-504-505-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTCG 55

Db 9 CTGGTCTCACCTCGCCATGGTTCG 32

RESULT 42

US-09-954-764-5

Sequence 5, Application US/09954764

Patent No. 6899879

GENERAL INFORMATION:

APPLICANT: DE BOER, MARK

APPLICANT: CONROY, LEAH B.

TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION

USING ANTI-CD40 MONOCLONAL ANTIBODIES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/954,764
FILING DATE: 18-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,893
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle, Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0925.003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-954-764-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGCTCTCACCTGCCCATGGTTCG 55
Db 9 CTGCTCTCACCTGCCCATGGTTCG 32

RESULT 43
US-07-910-222B-6/c
Sequence 6, Application US/07910222B
Patent No. 5397703
GENERAL INFORMATION:
APPLICANT: de Boer, Mark
APPLICANT: Conroy, Leah B.
TITLE OF INVENTION: A Method for Generation of Antibodies to
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Oncology Corporation
STREET: 1400 53rd Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/910,222B
FILING DATE: 19920709
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 2255-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3300
TELEFAX: (510) 658-5470
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Backward Primer for CD40, MR112
US-07-910-222B-6

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGTGG 905
Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 44
US-06-070-158-6/c
Sequence 6, Application US/08070158
Patent No. 5677165
GENERAL INFORMATION:
APPLICANT: DE BOER, MARK
APPLICANT: CONROY, LEAH B.
TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,158
FILING DATE: 28-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle, Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0925.003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-06-070-158-6

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGCG 905
Db 34 GGCTGCACCCACCCAGGAGTGCG 11

RESULT 45

US-08-200-716-6/c
; Sequence 6, Application US/08200716
; Patent No. 5747034
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods and Materials for Induction
; TITLE OF INVENTION: of T Cell Anergy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,716
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-716-6

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGCG 905
Db 34 GGCTGCACCCACCCAGGAGTGCG 11

Search completed: February 5, 2006, 12:22:42
Job time : 226 secs

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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:35:04 ; Search time 876 Seconds
(without alignments)
9477.689 Million cell updates/sec

Title: US-10-698-689-85
Perfect score: 1004
Sequence: 1 gctcgctcgccgcccagt.....ccagtcagtcgcccgcctc 1004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.0	50	6	US-10-131-827-108 Sequence 108, App
2	50	5.0	50	6	US-10-131-827-2096 Sequence 2096, App
3	33	3.3	40	3	US-09-844-684-1 Sequence 1, Appli
4	33	3.3	40	5	US-10-040-244-1 Sequence 1, Appli
5	33	3.3	40	7	US-10-693-629-1 Sequence 1, Appli
6	27	2.7	27	9	US-10-708-204-5523 Sequence 5523, App
7	27	2.7	27	9	US-10-708-204-5526 Sequence 5526, App
8	27	2.7	27	9	US-10-708-204-5539 Sequence 5539, App
9	27	2.7	30	9	US-10-708-204-5537 Sequence 5537, App
10	26	2.6	26	9	US-10-708-204-5530 Sequence 5530, App
11	25	2.5	25	3	US-09-067-638B-88 Sequence 88, Appli
12	25	2.5	25	5	US-10-116-325-88 Sequence 88, Appli
13	25	2.5	25	5	US-10-234-764-14 Sequence 14, Appli
14	25	2.5	25	6	US-10-388-263-88 Sequence 88, Appli
15	25	2.5	25	7	US-10-719-956-21131 Sequence 21131, A
16	25	2.5	25	8	US-10-698-689-88 Sequence 88, Appli
17	25	2.5	25	8	US-10-830-475-88 Sequence 88, Appli
18	25	2.5	25	8	US-10-649-467-88 Sequence 88, Appli
19	25	2.5	25	9	US-10-809-189-44613 Sequence 44613, A
20	25	2.5	25	9	US-10-809-189-44614 Sequence 44614, A
21	25	2.5	25	9	US-10-809-189-44615 Sequence 44615, A
22	25	2.5	25	9	US-10-809-189-44616 Sequence 44616, A
23	25	2.5	25	9	US-10-809-189-44617 Sequence 44617, A

US-10-809-189-44618 Sequence 44618, A
US-10-809-189-44619 Sequence 44619, A
US-10-809-189-44620 Sequence 44620, A
US-10-809-189-44621 Sequence 44621, A
US-10-809-189-44622 Sequence 44622, A
US-10-809-189-44623 Sequence 44623, A
US-10-809-189-44624 Sequence 44624, A
US-10-809-189-44625 Sequence 44625, A
US-10-809-189-44626 Sequence 44626, A
US-10-809-189-44627 Sequence 44627, A
US-10-809-189-44628 Sequence 44628, A
US-10-809-189-44629 Sequence 44629, A
US-10-809-189-44630 Sequence 44630, A
US-10-809-189-44631 Sequence 44631, A
US-10-809-189-44632 Sequence 44632, A
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US-10-956-157-137990 Sequence 137990, A
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US-10-956-157-140364 Sequence 140364, A
US-10-956-157-142216 Sequence 142216, A
US-10-956-157-147050 Sequence 147050, A
US-10-956-157-147541 Sequence 147541, A
US-10-956-157-148709 Sequence 148709, A
US-10-956-157-149025 Sequence 149025, A
US-10-956-157-152515 Sequence 152515, A
US-10-956-157-156126 Sequence 156126, A
US-10-956-157-156934 Sequence 156934, A
US-10-956-157-159114 Sequence 159114, A
US-10-956-157-161248 Sequence 161248, A
US-10-956-157-162815 Sequence 162815, A
US-10-956-157-164574 Sequence 164574, A
US-10-956-157-171041 Sequence 171041, A
US-10-956-157-171273 Sequence 171273, A
US-10-956-157-173732 Sequence 173732, A
US-10-956-157-173782 Sequence 173782, A
US-10-956-157-177050 Sequence 177050, A
US-10-956-157-177729 Sequence 177729, A
US-10-956-157-190834 Sequence 190834, A
US-10-956-157-192288 Sequence 192288, A
US-10-956-157-199366 Sequence 199366, A
US-10-956-157-200493 Sequence 200493, A
US-10-956-157-201329 Sequence 201329, A
US-10-956-157-202108 Sequence 202108, A
US-10-956-157-207083 Sequence 207083, A

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97 25 2.5 25 9 US-10-956-157-208396 Sequence 208396,
98 25 2.5 25 9 US-10-956-157-214493 Sequence 214493,
99 25 2.5 25 9 US-10-956-157-216269 Sequence 216269,
100 25 2.5 25 9 US-10-956-157-216847 Sequence 216847,
101 25 2.5 25 9 US-10-956-157-216948 Sequence 216948,
102 25 2.5 25 9 US-10-956-157-220091 Sequence 220091,
103 25 2.5 25 9 US-10-956-157-224317 Sequence 224317,
104 25 2.5 25 9 US-10-956-157-224555 Sequence 224555,
105 25 2.5 25 9 US-10-956-157-227012 Sequence 227012,
106 25 2.5 25 9 US-10-956-157-228559 Sequence 228559,
107 25 2.5 25 9 US-10-956-157-229038 Sequence 229038,
108 25 2.5 25 9 US-10-956-157-233044 Sequence 233044,
109 25 2.5 25 9 US-10-956-157-234558 Sequence 234558,
110 25 2.5 25 9 US-10-956-157-235109 Sequence 235109,
111 25 2.5 25 9 US-10-956-157-236430 Sequence 236430,
112 25 2.5 25 9 US-10-956-157-237395 Sequence 237395,
113 25 2.5 25 9 US-10-956-157-244333 Sequence 244333,
114 25 2.5 25 9 US-10-956-157-248301 Sequence 248301,
115 25 2.5 25 9 US-10-956-157-250791 Sequence 250791,
116 25 2.5 25 9 US-10-956-157-253095 Sequence 253095,
117 25 2.5 25 9 US-10-956-157-254460 Sequence 254460,
118 25 2.5 25 9 US-10-956-157-254926 Sequence 254926,
119 25 2.5 25 9 US-10-956-157-258924 Sequence 258924,
120 25 2.5 25 9 US-10-956-157-263956 Sequence 263956,

ALIGNMENTS

RESULT 1
US-10-131-827-108
; Sequence 108, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-108
Query Match 5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 827 GGTCAACCAGGAGTGGCAAGAGATCGCATCTCAGTGCAGGAGAC 876
Db 1 GGTCAACCAGGAGTGGCAAGAGATCGCATCTCAGTGCAGGAGAC 50

RESULT 2
US-10-131-827-2096
; Sequence 2096, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-108
Query Match 5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 827 GGTCAACCAGGAGTGGCAAGAGATCGCATCTCAGTGCAGGAGAC 876
Db 1 GGTCAACCAGGAGTGGCAAGAGATCGCATCTCAGTGCAGGAGAC 50

RESULT 3
US-09-844-684-1
; Sequence 1, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-844-684-1
Query Match 3.3%; Score 33; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCCATCCAGAACCAACCACCTGCATGCAGAG 129
Db 8 CTGTCCATCCAGAACCAACCACCTGCATGCAGAG 40

RESULT 4
US-10-040-244-1
; Sequence 1, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2096
Query Match 5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 834 CAGGAGATGGCAAGAGATCGCATCTCAGTGCAGGAGACAGTGAGG 883
Db 1 CAGGAGATGGCAAGAGATCGCATCTCAGTGCAGGAGACAGTGAGG 50

RESULT 3
US-09-844-684-1
; Sequence 1, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-844-684-1
Query Match 3.3%; Score 33; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCCATCCAGAACCAACCACCTGCATGCAGAG 129
Db 8 CTGTCCATCCAGAACCAACCACCTGCATGCAGAG 40

RESULT 4
US-10-040-244-1
; Sequence 1, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
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; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-040-244-1

Query Match 3.3%; Score 33; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCCATCCAGAACCCACTGTCATGCAGAG 129
Db 8 CTGTCCATCCAGAACCCACTGTCATGCAGAG 40

RESULT 5

US-10-693-629-1
; Sequence 1, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-693-629-1

Query Match 3.3%; Score 33; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCCATCCAGAACCCACTGTCATGCAGAG 129
Db 8 CTGTCCATCCAGAACCCACTGTCATGCAGAG 40

RESULT 6

US-10-708-204-5523
; Sequence 5523, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5523
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5523

Query Match 2.7%; Score 27; DB 9; Length 27;
Best Local Similarity 77.8%; Pred. No. 4.1e+02;
Matches 21; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 761 TCCCGACGATCTTCTGCTCAACAC 787
Db 1 UCCCGACGATCTTCTGCTCAACAC 27

RESULT 7

US-10-708-204-5526
; Sequence 5526, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5526
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5526

Query Match 2.7%; Score 27; DB 9; Length 27;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 829 TCACCCAGGAGTGGCAAGAGATC 855
Db 1 UCACCCAGGAGGAGGCAAGAGAGUC 27

RESULT 8

US-10-708-204-5539
; Sequence 5539, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5539
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5539

Query Match 2.7%; Score 27; DB 9; Length 27;

Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 828 GTCACCCAGGAGGATGCGAAGAGAGT 854
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Db 1 GUCACCCAGGAGGAGGCGAAGAGAGU 27

RESULT 9
US-10-708-204-5537/c
; Sequence 5537, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5537
; LENGTH: 30
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5537

Query Match 2.7%; Score 27; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 978 GCTATGCCAGTCAGTGCAGCCCTC 1004
|:|||||:|||||:|||||:|||||:|||||:
Db 30 GCTATGCCAGTCAGTGCAGCCCTC 4

RESULT 10
US-10-708-204-5530
; Sequence 5530, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5530
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5530

Query Match 2.6%; Score 26; DB 9; Length 26;
Best Local Similarity 80.8%; Pred. No. 8.5e+02;
Matches 21; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 762 CCCGACGATCTCTCGTGCCTCCACAC 787
|:|||||:|||||:|||||:|||||:|||||:
Db 1 CCCGACGAUCCUCCUGGCCUCCACAC 26

RESULT 11
US-09-067-638B-88
; Sequence 88, Application US/09067638B
; Patent No. US2002028923A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowert
; APPLICANT: Brenda F. Baker

APPLICANT: John McNeil
APPLICANT: Susan M. Preier
APPLICANT: Henri M. Sasnor
APPLICANT: Douglas G. Brooks
APPLICANT: Cara Ohashi
APPLICANT: Jacqueline R. Wyatt
APPLICANT: Alexander Borchers
APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Identification of Genetic
TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and
TITLE OF INVENTION: Generation of Oligonucleotides for Gene
TITLE OF INVENTION: Modulation
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOODCOCK WASHBURN KURTZ
ADDRESSEE: MACKIEWICZ & NORRIS LLP
STREET: 1 LIBERTY PLACE 46TH FLOOR
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM
OPERATING SYSTEM: PC-Windows NT
SOFTWARE: WORD PERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,638B
FILING DATE: 28-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/081,483
FILING DATE: 13-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-067-638B-88

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTCGGGTGAAAGCGAATTCCT 250
|:|||||:|||||:|||||:|||||:|||||:
Db 1 TTCCTTCGGGTGAAAGCGAATTCCT 25

RESULT 12
US-10-116-325-88
; Sequence 88, Application US/10116325
; Publication No. US20030113739A1
; GENERAL INFORMATION:
; APPLICANT: Cowert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Preier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets For Modulation By Oligonucleotides

```
; TITLE OF INVENTION: Generation Of Oligonucleotides For Gene Modulation
; FILE REFERENCE: ISIS5086
; CURRENT APPLICATION NUMBER: US/10/116,325
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030113739A1el Sequence
US-10-116-325-88

Query Match          2.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TTCCTTGGCGTGAAGCGGAATTCCT 250
Db 1 TTCCTTGGCGTGAAGCGGAATTCCT 25

RESULT 13
US-10-234-764-14
; Sequence 14, Application US/10234764
; Publication No. US20030113769A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Virta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS5089
; CURRENT APPLICATION NUMBER: US/10/234,764
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 09/344,260
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-234-764-14

Query Match          2.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TTCCTTGGCGTGAAGCGGAATTCCT 250
Db 1 TTCCTTGGCGTGAAGCGGAATTCCT 25

RESULT 14
US-10-388-263-88
; Sequence 88, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freiler, Susan M.
; APPLICANT: Sasmor, Henri M.
```

```
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-388-263-88

Query Match          2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TTCCTTGGCGTGAAGCGGAATTCCT 250
Db 1 TTCCTTGGCGTGAAGCGGAATTCCT 25

RESULT 15
US-10-719-956-21131
; Sequence 21131, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-21131

Query Match          2.5%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 AACACTGCTGCTCCAGTCGAGGAGA 807
Db 1 AACACTGCTGCTCCAGTCGAGGAGA 25

RESULT 16
US-10-698-689-88
; Sequence 88, Application US/10698689
; Publication No. US20040186071A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Malik, Leila
; APPLICANT: Siwkowski, Andrew
; APPLICANT: Eldrup, Anne B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 EXPRESSION
; FILE REFERENCE: ISIS-5315
; CURRENT APPLICATION NUMBER: US/10/698,689
; CURRENT FILING DATE: 2003-10-31
```

; PRIOR APPLICATION NUMBER: PCT/US03/31166
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 10/261,382
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-698-689-88

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred.No.1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAAGCGAATTCTT 250
|||||
Db 1 TTCCTTGGGTGAAAGCGAATTCTT 25

RESULT 17

US-10-830-475-88
; Sequence 88, Application US/10830475
; Publication No. US20040197814A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; Brenda F. Baker
; John McNeil
; Susan M. Freier
; Henri M. Sasmor
; Douglas G. Brooks
; Cara Ohashi
; Jacqueline R. Wyatt
; Alexander Borchers
; Timothy A. Vickers

TITLE OF INVENTION: Identification of Genetic
Targets for Modulation By Oligonucleotides and
Generation of Oligonucleotides for Gene
Modulation

NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOODCOCK WASHBURN KURTZ
MACKIEWICZ & NORRIS LLP
STREET: 1 LIBERTY PLACE 46TH FLOOR
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM
OPERATING SYSTEM: PC-Windows NT
SOFTWARE: WORD PERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/830,475
FILING DATE: 21-Apr-2004
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/067,638B
FILING DATE: 28-APR-1998
APPLICATION NUMBER: 60/081,483
FILING DATE: 13-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2960

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-830-475-88

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred.No.1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAAGCGAATTCTT 250
|||||
Db 1 TTCCTTGGGTGAAAGCGAATTCTT 25

RESULT 18

US-10-649-467-88
; Sequence 88, Application US/10649467
; Publication No. US20050033524A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; APPLICANT: Brenda F. Baker
; APPLICANT: John McNeil
; APPLICANT: Susan M. Freier
; APPLICANT: Henri M. Sasmor
; APPLICANT: Douglas G. Brooks
; APPLICANT: Cara Ohashi
; APPLICANT: Jacqueline R. Wyatt
; APPLICANT: Alexander Borchers
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotides for Gene Modulation
; FILE REFERENCE: ISIS0085-100 (ISIS2960US.C2)
; CURRENT APPLICATION NUMBER: US/10/649,467
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 09/067,636
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligomeric compound
US-10-649-467-88

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred.No.1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAAGCGAATTCTT 250
|||||
Db 1 TTCCTTGGGTGAAAGCGAATTCTT 25

RESULT 19

US-10-809-189-44613
; Sequence 44613, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44613

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGGTTCGTCCTGCTGCGTGG 72
|||||
Db 1 ATGGTTCGTCCTGCTGCGTGG 25

RESULT 20
US-10-809-189-44614
; Sequence 44614, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44614

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CGTCTGCTCTGCGTGGTCTCT 78
|||||
Db 1 CGTCTGCTCTGCGTGGTCTCT 25

RESULT 21
US-10-809-189-44615
; Sequence 44615, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44615
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44615

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 TTGTGCCAGCCAGGACAGAACTGG 189
|||||
Db 1 TTGTGCCAGCCAGGACAGAACTGG 25

RESULT 22
US-10-809-189-44616
; Sequence 44616, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44616

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GACTGCACAGAGTTCACTGAAACGG 219
|||||
Db 1 GACTGCACAGAGTTCACTGAAACGG 25

RESULT 23
US-10-809-189-44617
; Sequence 44617, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 44617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44617

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 GAAACGGAATCCTTCTCGGTG 237
Db 1 GAAACGGAATCCTTCTCGGTG 25

RESULT 24
US-10-809-189-44618
; Sequence 44618, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44618

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 GAATGCCTTCTTCCGCGTGAAGCG 243
Db 1 GAATGCCTTCTTCCGCGTGAAGCG 25

RESULT 25
US-10-809-189-44619
; Sequence 44619, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44619

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 TGCCTTCCTTGGCGTGAAGCGAAT 246
Db 1 TGCCTTCCTTGGCGTGAAGCGAAT 25

RESULT 26
US-10-809-189-44620
; Sequence 44620, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44620
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44620

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 240 AGCGAATTCCTAGACACCTGGAACA 264
Db 1 AGCGAATTCCTAGACACCTGGAACA 25

RESULT 27
US-10-809-189-44621
; Sequence 44621, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44621

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 243 GAATTCCTAGACACCTGGACAG 267
|||||
Db 1 GAATTCCTAGACACCTGGACAG 25

RESULT 28
US-10-809-189-44622
; Sequence 44622, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44622

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 AGAGAGACACTGCCACGACCA 288
|||||
Db 1 AGAGAGACACTGCCACGACCA 25

RESULT 29
US-10-809-189-44623
; Sequence 44623, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44623
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44623

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CACTGCCACGACCAATACTGCG 297
|||||
Db 1 CACTGCCACGACCAATACTGCG 25

RESULT 30
US-10-809-189-44624
; Sequence 44624, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44624

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 TGCCACCAGCACAATACTGCGACC 300
|||||
Db 1 TGCCACCAGCACAATACTGCGACC 25

RESULT 31
US-10-809-189-44625
; Sequence 44625, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44625

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 CTGCTCTGCAGTGCCTCTCTGGG 81
|||||
Db 1 CTGCTCTGCAGTGCCTCTCTGGG 25

RESULT 32
US-10-809-189-44626
; Sequence 44626, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:

```
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44626
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Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 CCTCTGCAGTGCCTCTCTGGGGCT 84
      |||||||
Db 1 CCTCTGCAGTGCCTCTCTGGGGCT 25
```

```
RESULT 33
US-10-809-189-44627
; Sequence 44627, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44627
```

```
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 CTGCAGTGCCTCTCTCTGGGGCTGT 87
      |||||||
Db 1 CTGCAGTGCCTCTCTCTGGGGCTGT 25
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RESULT 34
US-10-809-189-44628
; Sequence 44628, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
```

```
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44628
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Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 TTGCTGACCGCTGTCCATCCAGAAC 111
      |||||||
Db 1 TTGCTGACCGCTGTCCATCCAGAAC 25
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RESULT 35
US-10-809-189-44629
; Sequence 44629, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44629
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Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CCCACTGCATGCAGAGAAAAACAGT 138
      |||||||
Db 1 CCCACTGCATGCAGAGAAAAACAGT 25
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RESULT 36
US-10-809-189-44630
; Sequence 44630, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
```

; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44630
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44630

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 TACCTAATAAACAGTCAGTGTGTT 162
Db 1 TACCTAATAAACAGTCAGTGTGTT 25

RESULT 37
US-10-809-189-44631
; Sequence 44631, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44631

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AACAGTCAGTCGTCTTTGTGTC 171
Db 1 AACAGTCAGTCGTCTTTGTGTC 25

RESULT 38
US-10-809-189-44632
; Sequence 44632, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44632

; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44632

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 TCTTTGTGCCAGCAGGACAGAAAC 186
Db 1 TCTTTGTGCCAGCAGGACAGAAAC 25

RESULT 39
US-10-956-157-22769
; Sequence 22769, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22769
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22769

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 585 AACAAAGACTGATGTTGTCTGTGTC 609
Db 1 AACAAAGACTGATGTTGTCTGTGTC 25

RESULT 40
US-10-956-157-22770
; Sequence 22770, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22770
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22770

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 582 ACACAAAGACTGATGTTGTCTGTG 606
Db 1 ACACAAAGACTGATGTTGTCTGTG 25

RESULT 41

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US-10-956-157-22771
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22773
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22771
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22771
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 581 CACAACAAGACTGATGTTGCTGCTG 605
Db 1 CACAACAAGACTGATGTTGCTGCTG 25
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RESULT 42
US-10-956-157-22772
; Sequence 22772, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22772
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22772
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 583 CACAACAAGACTGATGTTGCTGCTG 607
Db 1 CACAACAAGACTGATGTTGCTGCTG 25
|||||
RESULT 43
US-10-956-157-22773
; Sequence 22773, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22773
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22773
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 583 CACAACAAGACTGATGTTGCTGCTG 607
Db 1 CACAACAAGACTGATGTTGCTGCTG 25
|||||
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; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22773
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 584 AAACAAGACTGATGTTGCTGCTGCTG 608
Db 1 AAACAAGACTGATGTTGCTGCTGCTG 25
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RESULT 44
US-10-956-157-22774
; Sequence 22774, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22774
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22774
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 580 GCACAACAAGACTGATGTTGCTGCTG 604
Db 1 GCACAACAAGACTGATGTTGCTGCTG 25
|||||
RESULT 45
US-10-956-157-22775
; Sequence 22775, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22775
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22775
Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 578 AGGCACAACAAGACTGATGTTGCTG 602
Db 1 AGGCACAACAAGACTGATGTTGCTG 25
|||||
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Job time : 877 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:46:00 ; Search time 394 Seconds

(without alignments)
2135.598 Million cell updates/sec

Title: US-10-698-689-85

Perfect score: 1004

Sequence: 1 gctcgtcgggcgccagtc.....ccagtcagtcgagccctc 1004

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 11560300

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

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- 2: /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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- 8: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgm2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	2.7	36	9	US-11-105-172-9
2	26.8	2.7	33	9	US-11-105-172-10
3	25	2.5	25	8	US-11-121-849-44635
4	25	2.5	25	8	US-11-121-849-44636
5	25	2.5	25	8	US-11-121-849-44637
6	25	2.5	25	8	US-11-121-849-44638
7	25	2.5	25	8	US-11-121-849-44639
8	25	2.5	25	8	US-11-121-849-44640
9	25	2.5	25	8	US-11-121-849-44641
10	25	2.5	25	8	US-11-121-849-44642
11	25	2.5	25	8	US-11-121-849-44643
12	25	2.5	25	8	US-11-121-849-44644
13	25	2.5	25	8	US-11-121-849-44645
14	25	2.5	25	8	US-11-121-849-44646
15	25	2.5	25	8	US-11-121-849-44647
16	25	2.5	25	8	US-11-121-849-44648
17	25	2.5	25	8	US-11-121-849-44649
18	25	2.5	25	8	US-11-121-849-44650
19	25	2.5	25	8	US-11-121-849-44651
20	25	2.5	25	8	US-11-121-849-44652
21	25	2.5	25	8	US-11-121-849-44653
22	25	2.5	25	8	US-11-121-849-44654

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96 19 1.9 19 9 US-11-101-244-1869 Sequence 1869, Ap
97 19 1.9 19 9 US-11-101-244-1870 Sequence 1870, Ap
98 19 1.9 19 9 US-11-101-244-82634 Sequence 82634, A
99 19 1.9 19 9 US-11-101-244-82635 Sequence 82635, A
100 19 1.9 19 9 US-11-101-244-82636 Sequence 82636, A
101 19 1.9 19 9 US-11-101-244-82637 Sequence 82637, A
102 19 1.9 19 9 US-11-101-244-82638 Sequence 82638, A
103 19 1.9 19 9 US-11-101-244-82639 Sequence 82639, A
104 19 1.9 19 9 US-11-101-244-82640 Sequence 82640, A
105 19 1.9 19 9 US-11-101-244-82642 Sequence 82642, A
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113 19 1.9 19 9 US-11-101-244-82653 Sequence 82653, A
114 19 1.9 19 9 US-11-101-244-82654 Sequence 82654, A
115 19 1.9 19 9 US-11-101-244-82655 Sequence 82655, A
116 19 1.9 19 9 US-11-101-244-82657 Sequence 82657, A
117 19 1.9 19 9 US-11-101-244-82658 Sequence 82658, A
118 19 1.9 19 9 US-11-101-244-82659 Sequence 82659, A
119 19 1.9 19 9 US-11-101-244-82660 Sequence 82660, A
120 19 1.9 19 9 US-11-101-244-82661 Sequence 82661, A
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ALIGNMENTS

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RESULT 1
US-11-105-172-9
; Sequence 9, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizermaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Primer 1160
US-11-105-172-9
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Query Match 2.7%; Score 27; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 42 CTCGCCATGGTTCCTCTGCTCTGCCTCTGCAG 68
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Db 10 CTCGCCATGGTTCCTCTGCTCTGCCTCTGCAG 36
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RESULT 2
US-11-105-172-10/c
; Sequence 10, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizermaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
```

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; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR FILING DATE: DE 102 47 755.8
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Primer 1161
US-11-105-172-10
```

```
Query Match 2.7%; Score 26.8; DB 9; Length 33;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 600 GTCTGTGTCCTCCAGGATCGCTGAGAGCC 629
| | | | | | | | | | | | | | | | | |
Db 33 GTCTGTGTCCTCCAGGATCGCTGAGATCC 4
```

```
RESULT 3
US-11-121-849-44635
; Sequence 44635, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44635
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of the artificial sequence: Primer 1161
US-11-121-849-44635
```

```
Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 375 CACTGTACGAGTGAGGCGCTGTGAGA 399
| | | | | | | | | | | | | | | | | |
Db 1 CACTGTACGAGTGAGGCGCTGTGAGA 25
```

```
RESULT 4
US-11-121-849-44636
; Sequence 44636, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44636
; LENGTH: 25
; TYPE: DNA
```

US-11-121-849-44639
; ORGANISM: Homo sapien
; Sequence 44639, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44637

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 390 GCCTGTGAGAGCTGTCTCTGCACC 414
|||||
Db 1 GCCTGTGAGAGCTGTCTCTGCACC 25

RESULT 5
US-11-121-849-44637
; Sequence 44637, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44637

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 AGCTGTGCTCTGCACCGTCTATGCT 423
|||||
Db 1 AGCTGTGCTCTGCACCGTCTATGCT 25

RESULT 6
US-11-121-849-44638
; Sequence 44638, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44638

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 420 TGCTGCCCCGGCTTTGGGTCAAGC 444
|||||
Db 1 TGCTGCCCCGGCTTTGGGTCAAGC 25

RESULT 7

US-11-121-849-44639
; Sequence 44639, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44639
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44639

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 439 TCAAGCAGATTGCTACAGGGGTTTC 463
|||||
Db 1 TCAAGCAGATTGCTACAGGGGTTTC 25

RESULT 8
US-11-121-849-44640
; Sequence 44640, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44640

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 TTCTGATACCATCTCGAGCCCTGC 485
|||||
Db 1 TTCTGATACCATCTCGAGCCCTGC 25

RESULT 9
US-11-121-849-44641
; Sequence 44641, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44641

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 TTCTGATACCATCTCGAGCCCTGC 485
|||||
Db 1 TTCTGATACCATCTCGAGCCCTGC 25

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44641

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GCCCAGTCGGTCTCTTCCCAATCT 508
|||||
Db 1 GCCCAGTCGGTCTCTTCCCAATCT 25

RESULT 10

US-11-121-849-44642
; Sequence 44642, Application US/11121849
; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44642
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-44642

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 498 TTCTCCAATGTCATCTGCTTCG 522
|||||
Db 1 TTCTCCAATGTCATCTGCTTCG 25

RESULT 11

US-11-121-849-44643
; Sequence 44643, Application US/11121849
; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-44643

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 ATGTGTCATCTGCTTTTCGAAAAATG 529
|||||

Db 1 ATGTGTCATCTGCTTTTCGAAAAATG 25

RESULT 12

US-11-121-849-44644
; Sequence 44644, Application US/11121849
; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-44644

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 519 TTCGAAAAATGTCACCTTCGACAA 543
|||||
Db 1 TTCGAAAAATGTCACCTTCGACAA 25

RESULT 13

US-11-121-849-44645
; Sequence 44645, Application US/11121849
; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-44645

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 579 GGCACAAACAAAGACTGATGTGTCT 603
|||||
Db 1 GGCACAAACAAAGACTGATGTGTCT 25

RESULT 14

US-11-121-849-44646
; Sequence 44646, Application US/11121849
; Publication No. US20050272080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44646
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44646

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 589 AGACTGATGTTCTCTGTGTCCTCCCA 613
|||||
Db 1 AGACTGATGTTCTCTGTGTCCTCCCA 25

RESULT 15

US-11-121-849-44647
; Sequence 44647, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44647

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 590 GACTGATGTTCTCTGTGTCCTCCAG 614
|||||
Db 1 GACTGATGTTCTCTGTGTCCTCCAG 25

RESULT 16

US-11-121-849-44648
; Sequence 44648, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44648

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 GCTGAGACCCCTGGTGGTATCCCC 644
|||||
Db 1 GCTGAGACCCCTGGTGGTATCCCC 25

RESULT 17

US-11-121-849-44649
; Sequence 44649, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44649

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 CCCTGGTGGTATCCCATCATCTT 652
|||||
Db 1 CCCTGGTGGTATCCCATCATCTT 25

RESULT 18

US-11-121-849-44650
; Sequence 44650, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44650

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 658 TCCTGTTTGCATCCTCTTGTGCT 682
|||||
Db 1 TCCTGTTTGCATCCTCTTGTGCT 25

RESULT 19

US-11-121-849-46828
; Sequence 46828, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46828

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      810 TTACATGGATGCCAACCGGTCACCC 834
Db      1 TTACATGGATGCCAACCGGTCACCC 25

RESULT 20
US-11-121-849-46829
; Sequence 46829, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46829
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46829

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      811 TACATGGATGCCAACCGGTCACCCA 835
Db      1 TACATGGATGCCAACCGGTCACCCA 25

RESULT 21
US-11-121-849-46830
; Sequence 46830, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46830
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46833
```

```
US-11-121-849-46830

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      812 ACATGGATGCCAACCGGTCACCCAG 836
Db      1 ACATGGATGCCAACCGGTCACCCAG 25

RESULT 22
US-11-121-849-46831
; Sequence 46831, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46831
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46831

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      813 CATGGATGCCAACCGGTCACCCAGG 837
Db      1 CATGGATGCCAACCGGTCACCCAGG 25

RESULT 23
US-11-121-849-46832
; Sequence 46832, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46832
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46832

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      889 CCCACCCAGGAGTGTGCCACCGTGG 913
Db      1 CCCACCCAGGAGTGTGCCACCGTGG 25

RESULT 24
US-11-121-849-46833
```

; Sequence 46833, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46833
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46833

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 CAGGAGTGGCCAGCTGGGCAAC 919
Db 1 CAGGAGTGGCCAGCTGGGCAAC 25
|||||

RESULT 25
US-11-121-849-46834
; Sequence 46834, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46834
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46834

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 GCAACAGCGCAGTTGGCCAGAGAGC 938
Db 1 GCAACAGCGCAGTTGGCCAGAGAGC 25
|||||

RESULT 26
US-11-121-849-46835
; Sequence 46835, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 46835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46835

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 CAAACAGCGCAGTTGGCCAGAGAGCC 939
Db 1 CAAACAGCGCAGTTGGCCAGAGAGCC 25
|||||

RESULT 27
US-11-121-849-46836
; Sequence 46836, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46836
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46836

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 AAACAGCGCAGTTGGCCAGAGAGCCT 940
Db 1 AAACAGCGCAGTTGGCCAGAGAGCCT 25
|||||

RESULT 28
US-11-121-849-46837
; Sequence 46837, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46837

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 AGGCAGTTGGCCAGAGAGCCTGGTG 944
Db 1 AGGCAGTTGGCCAGAGAGCCTGGTG 25
|||||

```
RESULT 29
US-11-121-849-46838
; Sequence 46838, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46838

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      922 GCAGTTGCCAGAGAGCCTGTGCT 946
Db      1 GCAGTTGCCAGAGAGCCTGTGCT 25

RESULT 30
US-11-121-849-141446
; Sequence 141446, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141446

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      786 ACTGCTGCTCCAGTGCAGGAGACTT 810
Db      1 ACTGCTGCTCCAGTGCAGGAGACTT 25

RESULT 31
US-11-121-849-141447
; Sequence 141447, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
```

```
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141447
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141447

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      823 AACCGTCCACCCAGGAGGATGGCAA 847
Db      1 AACCGTCCACCCAGGAGGATGGCAA 25

RESULT 32
US-11-121-849-141448
; Sequence 141448, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141448
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141448

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      824 ACCGTCACCCAGGAGGATGGCAA 848
Db      1 ACCGTCACCCAGGAGGATGGCAA 25

RESULT 33
US-11-121-849-141449
; Sequence 141449, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141449
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141449

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 826 CGGTACCCAGGAGGATGCAAGA 850
Db 1 CGGTACCCAGGAGGATGCAAGA 25

RESULT 34

US-11-121-849-141450
; Sequence 141450, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141450

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 GTCACCCAGGAGGATGCAAGA 852
Db 1 GTCACCCAGGAGGATGCAAGA 25

RESULT 35

US-11-121-849-141451
; Sequence 141451, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141451

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GATGCAAGAGATGCGATCTCAG 864
Db 1 GATGCAAGAGATGCGATCTCAG 25

RESULT 36

US-11-121-849-141452
; Sequence 141452, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141452
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141452

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 843 GCGAAGAGATGCGATCTCAGTC 867
Db 1 GCGAAGAGATGCGATCTCAGTC 25

RESULT 37

US-11-121-849-141453
; Sequence 141453, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141453

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 AAGAGATGCGATCTCAGTCAGGA 871
Db 1 AAGAGATGCGATCTCAGTCAGGA 25

RESULT 38

US-11-121-849-141454
; Sequence 141454, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141454
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141454

```
Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      849 GAGAGTCGATCTCTCAGTCGAGGAGA 873
      |||||
Db      1 GAGAGTCGATCTCTCAGTCGAGGAGA 25

RESULT 39
US-11-121-849-141455
; Sequence 141455, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141455

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      851 GAGTCGCATCTCTCAGTCGAGGAGA 875
      |||||
Db      1 GAGTCGCATCTCTCAGTCGAGGAGA 25

RESULT 40
US-11-121-849-141456
; Sequence 141456, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141456

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      873 AGACAGTGAGCTGCACCCACCCAG 897
      |||||
Db      1 AGACAGTGAGCTGCACCCACCCAG 25

RESULT 41
US-11-121-849-405290
; Sequence 405290, Application US/11121849
```

```
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 405290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-405290

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      873 AGACAGTGAGCTGCACCCACCCAG 897
      |||||
Db      1 AGACAGTGAGCTGCACCCACCCAG 25

RESULT 42
US-11-121-849-405291/c
; Sequence 405291, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 405291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-405291

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      975 GGAGCTATGCCAGTCAGTCGCCAGC 999
      |||||
Db      25 GGAGCTATGCCAGTCAGTCGCCAGC 1

RESULT 43
US-11-136-527-244207
; Sequence 244207, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 244207
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-244207

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  847 AAGAGAGTCGCATCTCAGTGCAGGA 871
      |||||
DB   1 AAGAGAGTCGCATCTCAGTGCAGGA 25

RESULT 44
US-10-924-074-18
; Sequence 18, Application US/10924074
; Publication No. US20050272050A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Bernstein, Jeanne
; APPLICANT: Eshel, Dani
; APPLICANT: Toporik, Amir
; APPLICANT: Chen, Aviva
; TITLE OF INVENTION: CD40 Splice Variants, Compositions for Making and Methods of
; FILE REFERENCE: 28800-501 CIP
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: PCT/IB03/0665
; PRIOR FILING DATE: 2003-02-23
; PRIOR APPLICATION NUMBER: 60/358,877
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-924-074-18

Query Match          2.4%; Score 24; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  373 GGCACGTACGAGTCAGCGCCTGTG 396
      |||||
DB   1 GGCACGTACGAGTCAGCGCCTGTG 24

RESULT 45
US-10-914A-402300
; Sequence 402300, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 402300
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-914A-402300

Query Match          2.4%; Score 24; DB 7; Length 24;
```

```
Best Local Similarity 95.8%; Pred. No. 7.3e+02;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  956 GGGGTGCGCAGCGCAGAAAGCGGGGAGC 979
      |||||
DB   1 GGGGUGCAGGCAGAGAGCGGGGAGC 24

Search completed: February 5, 2006, 12:44:19
Job time : 395 secs
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 08:42:01 ; Search time 5162 Seconds
(without alignments)
11055.952 Million cell updates/sec

Title: US-10-698-689-85
Perfect score: 1004
Sequence: 1 gctcgcctcgccgcagcgt.....ccagtcagtcgacgccctc 1004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : GenBank:
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_hcg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	3.3	40	6	BD182308
2	33	3.3	40	6	AX327715
3	28	2.8	28	6	AR090351
4	28	2.8	28	6	AR090352
5	28	2.8	28	6	AR197386
6	28	2.8	28	6	AR197387
7	28	2.8	28	6	AR259540
8	28	2.8	28	6	AR259541
9	27	2.7	36	6	CQ803276
10	26.8	2.7	33	6	CQ803277
11	25	2.5	25	6	AR138078
12	25	2.5	25	6	BD226629
13	25	2.5	25	6	BD250534
14	25	2.5	25	6	AR343051
15	25	2.5	25	6	AR611142
16	25	2.5	33	6	AX746460
17	25	2.5	33	6	AX763806
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	26	24	2.4	24	6	AX823741	Sequence
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	36	24	2.4	34	6	AR032330	Sequence
	37	24	2.4	34	6	AR095274	Sequence
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	50	23	2.3	23	6	AR611140	Sequence
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	54	22.2	2.2	23	6	AR254529	Sequence
	55	22.2	2.2	46	6	AX405389	Sequence
	56	22.2	2.2	50	6	CQ004016	Sequence
	57	22.2	2.2	50	6	CQ004366	Sequence
	58	22.2	2.2	50	6	CQ004370	Sequence
	59	22	2.2	50	6	AX823744	Sequence
	60	21.6	2.2	47	6	AR284477	Sequence
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	69	21	2.1	49	6	CQ970233	Sequence
	70	20.6	2.1	21	6	AR529574	Sequence
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	72	20.6	2.1	42	6	BD209058	Enzymatic
	73	20.6	2.1	47	6	AR289089	Sequence
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	75	20.6	2.1	50	6	CQ006589	Sequence
	76	20.4	2.0	42	6	BD203540	Method an
	77	20.4	2.0	50	6	AX233404	Sequence
	78	20.2	2.0	21	6	BD211594	Canine an
	79	20.2	2.0	21	6	AR241572	Sequence
	80	20.2	2.0	21	6	AR254528	Sequence
	81	20.2	2.0	46	6	AR4907	Sequence
	82	20.2	2.0	46	6	AR399747	Sequence
	83	20.2	2.0	47	6	AR290814	Sequence
	84	20.2	2.0	49	6	AR211086	Sequence
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	88	20	2.0	20	6	AX406772	Sequence
	89	20	2.0	20	6	AX746095	Sequence
	90	20	2.0	20	6	AX770446	Sequence
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92	20	2.0	42	6	BD203465	BD203465 Method an
93	20	2.0	42	6	BD209202	BD209202 Enzymatic
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c 96	19.8	2.0	24	6	AK652475	AK652475 Sequence
c 97	19.8	2.0	41	6	AX516027	AX516027 Sequence
c 98	19.8	2.0	41	6	AX518057	AX518057 Sequence
c 99	19.8	2.0	50	6	AX164884	AX164884 Sequence
c 100	19.8	2.0	50	6	AX164911	AX164911 Sequence
101	19.6	2.0	29	6	BD273625	BD273625 Materials
102	19.6	2.0	29	6	BD273645	BD273645 Materials
c 103	19.6	2.0	29	6	AK322271	AK322271 Sequence
c 104	19.6	2.0	35	6	BD169143	BD169143 BHLH-PAS
c 105	19.6	2.0	35	6	BD188203	BD188203 BHLH-PAS
c 106	19.6	2.0	42	6	BD201771	BD201771 Method an
c 107	19.6	2.0	42	6	BD203472	BD203472 Method an
c 108	19.6	2.0	50	6	BD273138	BD273138 Oral immu
c 109	19.6	2.0	50	6	C0007044	C0007044 Sequence
c 110	19.6	2.0	50	6	AX093084	AX093084 Sequence
c 111	19.4	1.9	21	6	AR580026	AR580026 Sequence
c 112	19.4	1.9	21	6	AR580027	AR580027 Sequence
c 113	19.4	1.9	45	8	S78949	S78949 T-cell rece
c 114	19.4	1.9	50	6	AK024001	AK024001 Sequence
c 115	19.4	1.9	50	6	AR032602	AR032602 Sequence
c 116	19.4	1.9	50	6	BD068875	BD068875 Enzymatic
c 117	19.4	1.9	50	6	C0005640	C0005640 Sequence
c 118	19.4	1.9	50	6	E12787	E12787 DNA probe f
c 119	19.4	1.9	50	6	I29342	I29342 Sequence 21
120	19.4	1.9	50	6	I91016	I91016 Sequence 21
ALIGNMENTS						
RESULT 1	BD182308	40 bp	DNA	linear	PAT 15-MAY-2003	
LOCUS	Anti CD40 monoclonal antibody.					
DEFINITION	BD182308					
ACCESSION	BD182308.1	GI:30793226				
VERSION	WO 02088186-A/1.					
KEYWORDS	synthetic construct					
SOURCE	other sequences; artificial sequences.					
ORGANISM	1 (bases 1 to 40)					
REFERENCE	Mikayama,T., Yoshida,H., Force,W.R., Chen,X. and Takahashi,N.					
AUTHORS	Anti CD40 monoclonal antibody					
TITLE	Patent: WO 02088186-A 1 07-NOV-2002;					
JOURNAL	KIRIN BREWERY CO LTD,TOSHIFUMI MIKAYAMA, HITOSHI YOSHIDA, WALKER R					
COMMENT	FORCE, XINGJIE CHEN,NOBUAKI TAKAHASHI					
	OS Artificial Sequence					
	PN WO 02088186-A/1					
	PF 07-NOV-2002					
	PD 26-APR-2002	WO 2002JP004292				
	PR 27-APR-2001	WO PCTUS0113672.11-MAY-2001	JP 01P	142482 PR		
	05-OCT-2001	JP 01P	310535.26-OCT-2001	US	10/040244 PI	
	TOSHIFUMI MIKAYAMA,HITOSHI YOSHIDA,WALKER					
	R FORCE,XINGJIE CHEN,					
	PI NOBUAKI TAKAHASHI					
	PC C07K16/28,C12N15/13,C12N5/10,C12P21/08,A61K39/395,A61P35/00,					
	PC A61P37/04,					
	PC A61P37/06,A61P37/08,A61P7/00					
	CC Description of Artificial Sequence:Synthetic DNA FH Key					
	Location/Qualifiers					
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Best Local Similarity 100.0%; Pred.No.1.5e+03;						
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	97	CTGTCCATCCAGAACCA	CCCACTGCATGCAGAG	129		
Db	8	CTGTCCATCCAGAACCA	CCCACTGCATGCAGAG	40		
RESULT 2						
AX327715	AX327715	40 bp	DNA	linear	PAT 07-JAN-2002	
LOCUS	Sequence 1 from Patent WO0183755.					
DEFINITION	AX327715					
ACCESSION	AX327715.1	GI:18098026				
VERSION	synthetic construct					
KEYWORDS	other sequences; artificial sequences.					
SOURCE	1					
ORGANISM	Mikayama,T., Takahashi,N., Chen,X. and Schoenberger,S.P.					
REFERENCE	Human anti-cd40 antibodies and methods of making and using same					
AUTHORS	Patent: WO 0183755-A 1 08-NOV-2001;					
TITLE	Gemini Science, Inc. (US)					
JOURNAL	Location/Qualifiers					
FEATURES	1..40					
source	/organism="synthetic construct"					
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	97	CTGTCCATCCAGAACCA	CCCACTGCATGCAGAG	129		
Db	8	CTGTCCATCCAGAACCA	CCCACTGCATGCAGAG	40		
RESULT 3						
AR090351	AR090351	28 bp	DNA	linear	PAT 07-SEP-2000	
LOCUS	Sequence 471 from patent US 5994076.					
DEFINITION	AR090351					
ACCESSION	AR090351.1	GI:10017106				
VERSION	Unknown.					
KEYWORDS	Unknown.					
SOURCE	Unclassified.					
ORGANISM	1 (bases 1 to 28)					
REFERENCE	Chenchik,A., Johadze,G. and Bibilashvili,R.					
AUTHORS	Methods of assaying differential expression					
TITLE	Patent: US 5994076-A 471 30-NOV-1999;					
JOURNAL	Location/Qualifiers					
FEATURES	1..28					
source	/organism="unknown"					
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ORIGIN						
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Best Local Similarity 100.0%; Pred.No.3.4e+04;						
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	198	TGCACAGAGTTCACTGA	ACCGAATGCC	225		
Db	1	TGCACAGAGTTCACTGA	ACCGAATGCC	28		
RESULT 4						
AR090352/c	AR090352	28 bp	DNA	linear	PAT 07-SEP-2000	
LOCUS						

[illegible]

LOCUS	CQ803276	36 bp	DNA	linear	PAT 10-MAY-2004
DEFINITION	Sequence 9 from Patent WO2004035794.				
ACCESSION	CQ803276				
VERSION	CQ803276.1	GI:47110174			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Pfizenmaier,K. and Wajant,H.				
TITLE	Selective, local activation of members of the tnfr ligand family of systemically inactive non-antibody tnfr ligand fusion proteins				
JOURNAL	Patent: WO 2004035794-A 9 29-APR-2004;				
FEATURES	Pfizenmaier, Klaus (DE); Wajant, Harald (DE)				
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Best Local Similarity	100.0%;	Pred. NO. 6.4e+04;			
Matches	27;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	42	CTGCCATGCTTCGTCGCTCTGCAG	68		
DB	10	CTGCCATGCTTCGTCGCTCTGCAG	36		
RESULT 10					
CQ803277/c					
LOCUS	CQ803277	33 bp	DNA	linear	PAT 10-MAY-2004
DEFINITION	Sequence 10 from Patent WO2004035794.				
ACCESSION	CQ803277				
VERSION	CQ803277.1	GI:47110175			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Pfizenmaier,K. and Wajant,H.				
TITLE	Selective, local activation of members of the tnfr ligand family of systemically inactive non-antibody tnfr ligand fusion proteins				
JOURNAL	Patent: WO 2004035794-A 10 29-APR-2004;				
FEATURES	Pfizenmaier, Klaus (DE); Wajant, Harald (DE)				
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Best Local Similarity	93.3%;	Pred. NO. 7.3e+04;			
Matches	28;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	600	GTCTGTGGTCCCGAGGATCGGCTGAGACC	629		
DB	33	GTCTGTGGTCCCGAGGATCGGCTGGGATCC	4		
RESULT 11					
AR138078					
LOCUS	AR138078	25 bp	DNA	linear	PAT 16-JUN-2001
DEFINITION	Sequence 88 from patent US 6197584.				
ACCESSION	AR138078				
VERSION	AR138078.1	GI:14479587			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				

modulation.
ACCESSION BD250534
VERSION BD250534.1 GI:33060304
SOURCE JP 2002511276-A/88.
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M., Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation
JOURNAL Patent: JP 2002511276-A 88 16-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002511276-A/88
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASNOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
C12N15/00
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FT source /organism='Artificial Sequence'.
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Location/Qualifiers
/organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 14
AR343051
LOCUS AR343051 25 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6576752.
ACCESSION AR343051
VERSION AR343051.1 GI:33738379
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers
JOURNAL Patent: US 6576752-A 14 10-JUN-2003;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 250
modulation.
ACCESSION BD250534
VERSION BD250534.1 GI:33060304
SOURCE JP 2002511276-A/88.
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M., Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation
JOURNAL Patent: JP 2002511276-A 88 16-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002511276-A/88
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASNOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
C12N15/00
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 14
AR343051
LOCUS AR343051 25 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6576752.
ACCESSION AR343051
VERSION AR343051.1 GI:33738379
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers
JOURNAL Patent: US 6576752-A 14 10-JUN-2003;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
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Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 250

|||||
DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 15
AR611142
LOCUS AR611142 25 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 14 from patent US 6825331.
ACCESSION AR611142
VERSION AR611142.1 GI:56666771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers, oligomer arrays and methods of using them
JOURNAL Patent: US 6825331-A 14 30-NOV-2004;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
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Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 16
AX746460
LOCUS AX746460 33 bp DNA linear PAT 20-JUN-2003
DEFINITION Sequence 9 from Patent EP1308167.
ACCESSION AX746460
VERSION AX746460.1 GI:32130727
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pickl,W.
TITLE Antigen presenting vesicles
JOURNAL Patent: EP 1308167-A 9 07-MAY-2003;
Pickl, Winfried, Ao. Univ. Prof. Dr. (AT)
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/organism="synthetic construct"
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ORIGIN
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Best Local Similarity 84.8%; Pred. No. 2.2e+05;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 95 CGCTGTCCATCCAGAACCCCACTGCATGCAG 127
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DB 1 CGCGGGGATCCCGAACCCCACTGCATGCAG 33
RESULT 17
AX763806
LOCUS AX763806 33 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 9 from Patent WO03039594.
ACCESSION AX763806

VERSION AX763806.1 GI:32258173
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
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AUTHORS Pickl,W., Derdak,S. and Seed,B.
TITLE Antigen presenting vesicles
JOURNAL Patent: WO 03039594-A 9 15-MAY-2003;
Pickl, Winfried, Ao. Univ. Prof. Dr. (AT) ; Derdak, Sophia (AT)
FEATURES Location/Qualifiers
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Best Local Similarity 84.8%; Pred. No. 2.2e+05;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 95 CGCTGTCATCCAGAACCCACCATGTCATGCAG 127
Db 1 CGCGGGGATCCGAGAACCCACCATGTCATGCAG 33
RESULT 18
AX093091/c
LOCUS AX093091 50 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 39 from Patent WO0118203.
ACCESSION AX093091
VERSION AX093091.1 GI:13509558
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dunstan,C.R., Wooden,S.K. and Mann,M.B.
TITLE Op9 fusion protein compositions and methods
JOURNAL Patent: WO 0118203-A 39 15-MAR-2001;
Angen Inc. (US)
FEATURES Location/Qualifiers
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Query Match 2.5%; Score 25; DB 6; Length 50;
Best Local Similarity 69.4%; Pred. No. 2.2e+05;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 466 ATACCATCTGGAGCCCTGCCAGTCGGCTTCTCTCCAATGTGTCTATC 514
Db 50 ACACCGTTGCAACGTTGCCGACGGTTCTTCTCCAGAACCTC 2
RESULT 19
CQ970331/c
LOCUS CQ970331 35 bp DNA linear PAT 20-DEC-2004
DEFINITION Sequence 2 from Patent WO2004046720.
ACCESSION CQ970331
VERSION CQ970331.1 GI:56744102
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ellmark,P., Furebring,C., Ohlin,M. and Borrebaeck,C.
TITLE Methods for identifying members of specific binding pairs

JOURNAL Patent: WO 2004046720-A 2 03-JUN-2004;
Alligator Bioscience AB (SE)
FEATURES Location/Qualifiers
source 1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CD40 cytoplasmic and transmembrane domain
oligonucleotide 2"
ORIGIN
Query Match 2.5%; Score 24.6; DB 6; Length 35;
Best Local Similarity 87.1%; Pred. No. 2.9e+05;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 859 TCTCAGTGCAGGAGACAGTGGCTGCAC 889
Db 35 TCTCAGTGCAGGAGACAGTGGCTGCACGC 5
RESULT 20
CQ970340/c
LOCUS CQ970340 35 bp DNA linear PAT 20-DEC-2004
DEFINITION Sequence 11 from Patent WO2004046720.
ACCESSION CQ970340
VERSION CQ970340.1 GI:56744111
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ellmark,P., Furebring,C., Ohlin,M. and Borrebaeck,C.
TITLE Methods for identifying members of specific binding pairs
JOURNAL Patent: WO 2004046720-A 11 03-JUN-2004;
Alligator Bioscience AB (SE)
FEATURES Location/Qualifiers
source 1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' CD40 (Sall) oligonucleotide"
ORIGIN
Query Match 2.5%; Score 24.6; DB 6; Length 35;
Best Local Similarity 87.1%; Pred. No. 2.9e+05;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 859 TCTCAGTGCAGGAGACAGTGGCTGCAC 889
Db 35 TCTCAGTGCAGGAGACAGTGGCTGCACGC 5
RESULT 21
CQ790416
LOCUS CQ790416 24 bp DNA linear PAT 29-MAR-2004
DEFINITION Sequence 37 from Patent WO2004022749.
ACCESSION CQ790416
VERSION CQ790416.1 GI:45823458
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hecker,M. and Wagner,A.H.
TITLE Decoy-oligonucleotide-inhibition of cd40-expression
JOURNAL Patent: WO 2004022749-A 37 18-MAR-2004;
Avontec GmbH (DE)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAAACGGAATGCC 225
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Db 1 CAGAGTTCACTGAAACGGAATGCC 24

RESULT 22
AX027448
LOCUS AX027448 24 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 1 from Patent WO039294.
ACCESSION AX027448
VERSION AX027448.1 GI:10188414
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Bravery,C., Thompson,S. and Rushworth,S.
TITLE Porcine cells incapable of expressing cd40 antigen, for xenotransplantation
JOURNAL Patent: WO 0039294-A 1 06-JUL-2000;
NOVARTIS ERFIND VERWALT GMBH (AT); NOVARTIS AG (CH); BRAVERY CHRISTOPHER (GB); THOMPSON SIMON (GB); RUSHWORTH STUART (GB)
LOCATION/Qualifiers

FEATURES
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer A"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 TCGGCTTCTTCCCAATGTGTCAT 513
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Db 1 TCGGCTTCTTCCCAATGTGTCAT 24

RESULT 23
AX0406771
LOCUS AX0406771 24 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 27 from Patent WO229044.
ACCESSION AX0406771
VERSION AX0406771.1 GI:21439696
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Hecker,M. and Wagner,A.H.
TITLE Modulation of the transcription of pro-inflammatory gene products
JOURNAL Patent: WO 0229044-A 27 11-APR-2002;
LOCATION/Qualifiers

FEATURES
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAAACGGAATGCC 225
|||||
Db 1 CAGAGTTCACTGAAACGGAATGCC 24

RESULT 26
AX823741
LOCUS AX823741 24 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 18 from Patent WO03070768.
ACCESSION AX823741
VERSION AX823741.1 GI:39750074
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1
REFERENCE Bernstein,J., Mintz,L. and Eshel,D.
AUTHORS Cd40 splice variants, compositions for making and methods of using
TITLE the same
JOURNAL Patent: WO 03070768-A 18 28-AUG-2003;
COMPUGEN Ltd. (IL)
FEATURES Location/Qualifiers
source
1. .32
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 373 GGCACGTGTACGAGTGAGGCGCTGTG 396
Db 1 GGCACGTGTACGAGTGAGGCGCTGTG 24
RESULT 27
LOCUS AR004297 32 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 5 from patent US 5747034.
ACCESSION AR004297
VERSION AR004297.1 GI:3965176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods and materials for the induction of T cell anergy
JOURNAL Patent: US 5747034-A 5 05-MAY-1998;
FEATURES Location/Qualifiers
source
1. .32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTGC 55
Db 9 CTGGTCTCACCTCGCCCATGGTTGC 32
RESULT 28
LOCUS AR004299 32 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 7 from patent US 5747034.
ACCESSION AR004299
VERSION AR004299.1 GI:3965178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods and materials for the induction of T cell anergy
JOURNAL Patent: US 5747034-A 7 05-MAY-1998;
FEATURES Location/Qualifiers
source
1. .32
/organism="unknown"

ORIGIN /mol_type="unassigned DNA"
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTGC 55
Db 9 CTGGTCTCACCTCGCCCATGGTTGC 32
RESULT 29
LOCUS AR032329 32 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5869050.
ACCESSION AR032329
VERSION AR032329.1 GI:5947934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal
JOURNAL antibodies
FEATURES Patent: US 5869050-A 5 09-FEB-1999;
Location/Qualifiers
source
1. .32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTGC 55
Db 9 CTGGTCTCACCTCGCCCATGGTTGC 32
RESULT 30
LOCUS AR032331 32 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5869050.
ACCESSION AR032331
VERSION AR032331.1 GI:5947936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal
JOURNAL antibodies
FEATURES Patent: US 5869050-A 7 09-FEB-1999;
Location/Qualifiers
source
1. .32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTGC 55
Db 9 CTGGTCTCACCTCGCCCATGGTTGC 32
RESULT 31

AR095273 LOCUS AR095273 32 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 5 from patent US 6004552.
ACCESSION AR095273
VERSION AR095273.1 GI:10022998
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking B cell proliferation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6004552-A 5 21-DEC-1999;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 32
LOCUS AR178093 32 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 5 from patent US 6315998.
ACCESSION AR178093
VERSION AR178093.1 GI:17920986
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking B-cell activation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6315998-A 5 13-NOV-2001;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 33
LOCUS I69320 32 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 5 from patent US 5677165.
ACCESSION I69320
VERSION I69320.1 GI:2831442
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Anti-CD40 monoclonal antibodies capable of blocking B-cell activation

JOURNAL Patent: US 5677165-A 5 14-OCT-1997;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 34
LOCUS AR659104 32 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 5 from patent US 6899879.
ACCESSION AR659104
VERSION AR659104.1 GI:67595032
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Method for treating an Ige-mediated disease in a patient using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6899879-A 5 31-MAY-2005;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 35
LOCUS AR004298 34 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5747034.
ACCESSION AR004298
VERSION AR004298.1 GI:3965177
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods and materials for the induction of T cell anergy
JOURNAL Patent: US 5747034-A 6 05-MAY-1998;
FEATURES Location/Qualifiers
1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCAGGAGTGTGG 905
|||||

Db 34 GGCTGCACCCACCAGGAGTGTGG 11

RESULT 36
LOCUS AR032330/c 34 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5869050.
ACCESSION AR032330
VERSION AR032330.1 GI:5947935
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal antibodies
JOURNAL Patent: US 5869050-A 6 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCAGGAGTGTGG 11

RESULT 37
LOCUS AR095274/c 34 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 6004552.
ACCESSION AR095274
VERSION AR095274.1 GI:10023000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Methods of blocking B cell proliferation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6004552-A 6 21-DEC-1999;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCAGGAGTGTGG 11

RESULT 38
LOCUS AR178094/c 34 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 6 from patent US 6315998.
ACCESSION AR178094
VERSION AR178094.1 GI:17920987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Method for treating an IgE-mediated disease in a patient using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6315998-A 6 31-MAY-2005;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;

REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Methods of blocking B-cell activation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6315998-A 6 13-NOV-2001;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCAGGAGTGTGG 11

RESULT 39
LOCUS I69321/c 34 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 6 from patent US 5677165.
ACCESSION I69321
VERSION I69321.1 GI:2831443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Anti-CD40 monoclonal antibodies capable of blocking B-cell activation
JOURNAL Patent: US 5677165-A 6 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCAGGAGTGTGG 11

RESULT 40
LOCUS AR659105/c 34 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 6 from patent US 6899879.
ACCESSION AR659105
VERSION AR659105.1 GI:67595033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Method for treating an IgE-mediated disease in a patient using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6899879-A 6 31-MAY-2005;
FEATURES Location/Qualifiers
source 1..34
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;

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Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GCGTCGACCCACCCAGGAGTGCG 905
Db 34 GCGTCGACCCACCCAGGAGTGCG 11

RESULT 41
ARI38076
LOCUS ARI38076 23 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 86 from patent US 6197584.
ACCESSION ARI38076
VERSION ARI38076.1 GI:14479585
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. Frank. and Cowsert, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 86 06-MAR-2001;
FEATURES
    source
        Location/Qualifiers
            1..23
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match 2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAACGGAATGC 224
Db 1 CAGAGTTCACTGAACGGAATGC 23

RESULT 42
ARI38077/c
LOCUS ARI38077 23 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 87 from patent US 6197584.
ACCESSION ARI38077
VERSION ARI38077.1 GI:14479586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. Frank. and Cowsert, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 87 06-MAR-2001;
FEATURES
    source
        Location/Qualifiers
            1..23
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Query Match 2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GAACAGAGACACACTGCCACC 282
Db 23 GAACAGAGACACACTGCCACC 1

RESULT 43
BD226627
LOCUS BD226627 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226627
VERSION BD226627.1 GI:33036397
KEYWORDS JP 2002513593-A/86.
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unidentified
unclassified.
1 (bases 1 to 23)
Bennett, C. F. and Cowsert, L. M.
Antisense modulation of CD40 expression
Patent: JP 2002513593-A 86 14-MAY-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002513593-A/86
PD 14-MAY-2002
PF 22-APR-1999 JP 2000547271
PR 01-MAY-1998 US 09/071433
PI C FRANK BENNETT, LEX M COWSERT
PC C12N15/09, A61K9/10, A61K45/00, A61K48/00, A61P1/00, A61P11/06, PC
A61P17/06,
PC A61P29/00, A61P35/00, A61P37/02, A61P37/06, A61P43/00, C12P19/34,
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of CD40 expression
FH Key 1..23 Location/Qualifiers
FT source /organism='Unidentified'.
FEATURES
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        Location/Qualifiers
            1..23
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
ORIGIN
Query Match 2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAACGGAATGC 224
Db 1 CAGAGTTCACTGAACGGAATGC 23

RESULT 44
BD226628/c
LOCUS BD226628 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226628
VERSION BD226628.1 GI:33036398
KEYWORDS JP 2002513593-A/87.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. F. and Cowsert, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: JP 2002513593-A 87 14-MAY-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002513593-A/87
PD 14-MAY-2002
PF 22-APR-1999 JP 2000547271
PR 01-MAY-1998 US 09/071433
PI C FRANK BENNETT, LEX M COWSERT
PC C12N15/09, A61K9/10, A61K45/00, A61K48/00, A61P1/00, A61P11/06, PC
A61P17/06,
PC A61P29/00, A61P35/00, A61P37/02, A61P37/06, A61P43/00, C12P19/34,
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of CD40 expression
FH Key 1..23 Location/Qualifiers
FT source /organism='Unidentified'.
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FEATURES
source Location/Qualifiers
1. .23
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GAACAGAGAGACACTGCCACC 282
|||||
Db 23 GAACAGAGAGACACTGCCACC 1

RESULT 45
BD250532
LOCUS 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene
modulation.
ACCESSION BD250532
VERSION BD250532.1 GI:33060302
KEYWORDS JP 2002511276-A/86.
SOURCE synthetic construct
ORGANISM
REFERENCE 1 (bases 1 to 23)
AUTHORS Cowsett,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene
modulation
JOURNAL Patent: JP 2002511276-A 86 16-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002511276-A/86
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSETT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASNOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
C12N15/00
CC PCR Primer Location/Qualifiers
FH Key 1. .23
FT source /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1. .23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACTGAACCGAATGC 224
|||||
Db 1 CAGAGTTCACTGAACCGAATGC 23

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 04:55:45 : Search time 648 Seconds

(without alignments)
10326.160 Million cell updates/sec

Title: US-10-698-689-85

Perfect score: 1004

Sequence: 1 gcctcgctggcgccagc.....ccagtcagtcgacgcccctc 1004

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database : N_Geneseq_21.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002as.*

7: geneseqn2002bs.*

8: geneseqn2003as.*

9: geneseqn2003bs.*

10: geneseqn2003cs.*

11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.0	50	6	ABZ00117 Human leu
2	50	5.0	50	6	ABZ002105
3	50	5.0	50	10	ADG33437
4	50	5.0	50	10	ADP10127
5	33	3.3	40	8	ABT31837
6	28	2.8	28	6	ABK66384
7	28	2.8	28	6	ABK66383
8	27.4	2.7	41	3	AAA50914
9	27	2.7	27	13	ADT51360
10	27	2.7	36	12	ADP20784
11	26.8	2.7	33	12	ADP20785
12	26.4	2.6	37	3	AAA50913
13	26	2.6	26	12	ADP12202
14	25	2.5	25	2	AZ40939
15	25	2.5	25	3	AZ47772
16	25	2.5	25	14	ADY75649
17	25	2.5	33	10	ADC79171
18	25	2.5	50	4	AA03093
19	24.6	2.5	35	12	ADO26914


```
CC  rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ  Sequence 50 BP; 16 A; 8 C; 20 G; 6 T; 0 U; 0 Other;
    Query Match          5.0%; Score 50; DB 6; Length 50;
    Best Local Similarity 100.0%; Pred. No. 0.00033;
    Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  834 CAGGAGGATGCCAAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 883
Db   1 CAGGAGGATGCCAAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 50

RESULT 3
ADG33437
ID  ADG33437 standard; DNA; 50 BP.
XX
AC  ADG33437;
XX
DT  26-FEB-2004 (first entry)
XX
DE  Human DNA probe used to monitor expression of diagnostic genes SegID761.
XX
KW  human; ss; autoimmune; chronic inflammatory disease; SLE;
KW  systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW  Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW  ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW  diverticulitis; primary biliary sclerosis; probe.
XX
OS  Homo sapiens.
XX
PN  WO2003090694-A2.
XX
PD  06-NOV-2003.
XX
PF  24-APR-2003; 2003WO-US013015.
XX
PR  24-APR-2002; 2002US-00131827.
XX
PA  (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI  Wohlgenuth J, Fry K, Woodward R, Ly N;
XX  WPI; 2003-877243/81.
XX
DR  Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
XX  such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
XX  colitis, psoriasis and asthma by detecting the expression level of one or
XX  more genes.
XX
PS  Claim 1; SEQ ID NO 761; 877pp; English.
XX
CC  This invention relates to novel methods for diagnosing and monitoring
XX  autoimmune and chronic inflammatory diseases. Specifically, it refers to
XX  the identification of genes that have a clinical utility as diagnostic
XX  tools for the management of, in particular, patients with systemic lupus
XX  erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
XX  present invention describes a method for determining the levels of
XX  multiple differentially expressed genes of a patient, in a concerted
XX  manner, in order to achieve an improved diagnostic assay with sensitivity
XX  and specificity for the disease in question. As such, these genes are
XX  useful for the diagnosis of various other inflammatory disorders
XX  including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
XX  ankylosing spondylitis, ulcerative colitis, primary sclerosing
XX  cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
XX  This oligonucleotide is a human DNA probe used to monitor the expression
XX  level of the differentially expressed diagnostic genes of the invention.
XX
SQ  Sequence 50 BP; 16 A; 8 C; 20 G; 6 T; 0 U; 0 Other;
    Query Match          5.0%; Score 50; DB 10; Length 50;
    Best Local Similarity 100.0%; Pred. No. 0.00033;
    Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY  834 CAGGAGGATGCCAAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 883
Db   1 CAGGAGGATGCCAAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 50

RESULT 4
ADP10127
ID  ADP10127 standard; DNA; 50 BP.
XX
AC  ADP10127;
XX
DT  12-AUG-2004 (first entry)
XX
DE  50-mer oligonucleotide marker probe of the invention #136.
XX
KW  transplant rejection; immune system; rheumatoid arthritis; lupus;
KW  inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS  Homo sapiens.
XX
PN  WO2004042346-A2.
XX
PD  21-MAY-2004.
XX
PF  24-APR-2003; 2003WO-US012946.
XX
PR  24-APR-2002; 2002US-00131831.
XX
PR  20-DEC-2002; 2002US-00325899.
XX
XX  (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI  Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX  Rosenberg S;
XX
DR  WPI; 2004-400724/37.
XX
PT  Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT  pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT  rejection, in an individual, comprises detecting the expression level of
PT  the genes.
XX
PS  Claim 2; SEQ ID NO 136; 1762pp; English.
XX
CC  The present invention relates to diagnosing or monitoring transplant
XX  rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX  comprises detecting the expression level of one or more genes. The
XX  methods, system and kits are useful in diagnosing or monitoring
XX  transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX  islet, lung, bone marrow or stem cell transplant rejection,
XX  xenotransplant rejection or mechanical organ replacement rejection, in an
XX  individual. The method is also useful in assessing the immune status of
XX  diseases that involve the immune system, e.g. rheumatoid arthritis,
XX  lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX  viral, bacterial or fungal infection. The present sequence represents a
XX  50 mer oligonucleotide marker for diagnosis and monitoring of allograft
XX  rejection and other disorders.
XX
SQ  Sequence 50 BP; 16 A; 8 C; 20 G; 6 T; 0 U; 0 Other;
    Query Match          5.0%; Score 50; DB 12; Length 50;
    Best Local Similarity 100.0%; Pred. No. 0.00033;
    Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY  834 CAGGAGGATGCCAAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 883
Db   1 CAGGAGGATGCCAAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 50

RESULT 5
ABT31837
ID  ABT31837 standard; DNA; 40 BP.
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XX AC ABT31837;
XX DT 01-MAY-2003 (first entry)
XX DE Anti-CD40 monoclonal antibody related oligo SEQ ID No 1.
XX KW Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
XX KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
XX KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
XX KW immunosuppressor; anti-tumour agent; immunosuppressant; allergy;
XX KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; ds.
XX OS Unidentified.
XX PN WO200288186-A1.
XX PD 07-NOV-2002.
XX PF 26-APR-2002; 2002WO-JP004292.
XX PR 27-APR-2001; 2001WO-US013672.
XX PR 11-MAY-2001; 2001JP-00142482.
XX PR 05-OCT-2001; 2001JP-00310535.
XX PR 26-OCT-2001; 2001US-00040244.
XX PA (KIRI ) KIRIN BEER KK.
XX PI Miyayama T, Yoshida H, Force WR, Chen X, Takahashi N;
XX DR WPI; 2003-120463/11.
XX PT Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
XX PT or functional fragment, is useful in the treatment of e.g. autoimmune
XX PT diseases or cancer.
XX PS Example 1; Page 24; 94pp; Japanese.
XX CC The invention relates to an antibody to human CD40, or its functional
XX CC fragment, has at least one of the following properties: acting on
XX CC dendritic cells to produce IL-12 in the presence of LPS
XX CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
XX CC cells to activate maturation of the dendritic cells with high G28-5
XX CC antibody; and activating CD95 expression with high G28-5 antibody against
XX CC B cell line. Such antibodies or functional fragments can be used as
XX CC immunosuppressors, anti-tumour agents, immunosuppressants, and as remedies
XX CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors
XX CC syndrome. This polynucleotide sequence represents an oligo relating to
XX CC the anti-CD40 monoclonal antibody of the invention
XX SQ Sequence 40 BP; 11 A; 16 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 3.3%; Score 33; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 CTGTCATCCAGACACCACTGTCATGCAG 129
Db 8 CTGTCATCCAGACACCACTGTCATGCAG 40

RESULT 6
ABK66384/c
ID ABK66384 standard; DNA; 28 BP.
XX AC ABK66384;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #472.
XX DE Primer; ss; DNA microarray; differential expression analysis; human.
XX KW US6352829-B1.
XX OS Homo sapiens.

OS Homo sapiens.
XX PN US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-00225928.
XX PR 21-MAY-1997; 97US-00859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Jokhadze G, Bibilashvili R;
XX DR WPI; 2002-314699/35.
XX PT Producing sub-population of labeled nucleic acids, useful for analyzing
XX PT differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers.
XX PS Example 3; SEQ ID NO 472; 11pp; English.
XX CC The invention relates to producing a sub-population of labeled nucleic
XX CC acids (NAs) comprising contacting a NA sample from a physiological
XX CC source, with a pool of 50 distinct gene specific primers under suitable
XX CC conditions to enzymatically generate sub-population of NAs, where each
XX CC gene specific primer has a sequence complementary to a distinct mRNA, and
XX CC each labeled NA is generated using a single gene specific primer. The
XX CC method is useful for producing a sub-population of labeled NAs which is
XX CC useful for analysing the differences in the RNA profiles between several
XX CC different physiological sources, where the method comprises producing
XX CC subpopulation of labeled NAs for the different physiological sources,
XX CC comprising the populations for each physiological source to identify
XX CC differences in the population, where the comparison is preferably
XX CC performed by hybridising the labeled NAs for each of the distinct
XX CC physiological sources to an array of probe NAs stably associated with the
XX CC surface of a substrate to produce a hybridisation pattern for each of the
XX CC sources, and comparing the patterns for each of the sources, where
XX CC differential gene expression assays are utilised in differential
XX CC expression analysis of diseased a normal tissue e.g. neoplastic a normal
XX CC tissue, or different tissue or subtype types. The present sequence is a
XX CC human gene specific PCR primer used in the method of the invention. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from USPTO
XX CC at http.wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1
XX SQ Sequence 28 BP; 6 A; 7 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 2.8%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 577 CAGGCACAAACAAAGACTGATGTTGCTG 604
Db 28 CAGGCACAAACAAAGACTGATGTTGCTG 1

RESULT 7
ABK66383
ID ABK66383 standard; DNA; 28 BP.
XX AC ABK66383;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #471.
XX DE Primer; ss; DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX KW US6352829-B1.
XX OS Homo sapiens.

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PA (AMBR//) TORRAS AMBROS J.
PA (ORTE//) PLUVINET ORTEGA R.
PA (GARR//) CRUZADO GARRIT J M.
PA (PRES//) HERRERO FRESNEDA I.
XX
PI Aran Perramon JM, Grinyo Boixa JM, Torras Ambros J;
PI Pluvinet Ortega R, Cruzado Garrit JM, Herrero Fresneda I;
XX
XX WPI; 2004-748766/73.
XX
XX New oligoribonucleotides specific for the human CD40 receptor, useful for
XX treating e.g. transplant rejection, inflammation and autoimmune diseases,
XX also related duplexes and gene transfer vectors.
XX
XX Disclosure; SEQ ID NO 13; 52pp; Spanish.
XX
XX The invention relates to oligoribonucleotide (ON1) homologous with the
XX 241-259 region of the cDNA (I) that encodes the human CD40 receptor,
XX published as GenBank X60592. ON1, also their subsequences and derived
XX duplexes (all optionally chemically modified), are useful for treatment
XX of rejection of transplanted organs or tissues; acute and chronic
XX inflammation; processes that involve co-stimulation of lymphocytes;
XX allergic, autoimmune or cardiovascular disorders; infections; rheumatoid
XX states and cancers, specifically allergic dermatitis; psoriasis;
XX arteriosclerosis; multiple sclerosis; pulmonary fibrosis; viral and
XX bacterial infection; asthma; type I diabetes; Lyme and Crohn diseases;
XX ulcerative colitis; lupus; thyroiditis; arthritis; leukemia and lymphoma;
XX also neurodegenerative diseases. This sequence corresponds to one of the
XX small interfering RNA (siRNA) molecules used as an example of the
XX oligonucleotides of the invention.
XX
XX Sequence 27 BP; 10 A; 7 C; 6 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 2.7%; Score 27; DB 13; Length 27;
XX Best Local Similarity 85.2%; Pred. No. 1.1e+03;
XX Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
QY 237 GAAAGCGAATTCCTAGACACCTGGAC 263
Db 1 GAAAGCGAATTCCTAGACACCTGGAC 27
XX
XX RESULT 10
XX ADP20784
XX ID ADP20784 standard; DNA; 36 BP.
XX AC ADP20784;
XX
XX 12-AUG-2004 (first entry)
XX
XX CD40ex-Flag-TRAILex PCR primer 1160.
XX
XX ss; binding domain; cell-surface molecule; tumour necrosis factor;
XX TNF ligand family; TRAIL; TNF receptor superfamily; cytostatic;
XX antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
XX neuroprotective; antidiabetic; protozoacide; virucide; antibacterial;
XX antiallergic; signalling cascade; apoptosis; immunomodulation; cancer;
XX metabolic disease; multiple sclerosis; diabetes mellitus;
XX transplant rejection.
XX
XX Synthetic.
XX
XX DE10247755-A1.
XX
XX 22-APR-2004.
XX
XX 14-OCT-2002; 2002DE-01047755.
XX
XX 14-OCT-2002; 2002DE-01047755.
XX
XX (PFIZ//) PFIZENMAIER K.
XX (WAJA//) WAJANT H.
XX
```

```
PI Pfizenmaier K, Wajant H;
XX
XX WPI; 2004-331870/31.
XX
XX New fusion polypeptide, useful for treating e.g. cancer, infections and
XX inflammation, comprises binding domain for cell-surface molecule and
XX fragment of tumor necrosis factor ligand.
XX
XX Example 1; Page 9; 16pp; German.
XX
XX This invention describes a novel polypeptide which comprises a segment
XX that contains a binding domain for a cell-surface molecule; a peptide
XX linker and a segment that contains a fragment of a member of the tumour
XX necrosis factor (TNF) ligand (TRAIL) family that, alone, is inactive or
XX has limited activity. The binding domain is not derived from an
XX immunoglobulin and the TRAIL fragment becomes fully active only after
XX binding of the binding domain to a cell-surface molecule. The TNF ligand
XX fragment is the extracellular domain (or its functional variants or
XX fragments) of a TNF family ligand, especially TRAIL, Fas, TNF, 41BBL,
XX CD40L, CD30L or OX40L. The binding domain binds to a membrane protein and
XX is at least the essential part of a ligand for a membrane-bound receptor,
XX specifically where the ligand is a peptide or protein hormone (especially
XX a growth factor, e.g. epidermal growth factor, or an angiogenic agent,
XX e.g. vascular endothelial growth factor) or a cytokine. Alternatively,
XX the binding domain is derived from a receptor, especially of the TNF
XX receptor superfamily, e.g. TNF-R2, CD30, CD40 or CD28, for a membrane-
XX bound ligand, provided that it does not bind to the extracellular domain
XX of the ligand from which TNF ligand segment is derived. The products of
XX the invention have cytostatic, antiinflammatory, immunosuppressive,
XX antirheumatic, antiarthritic, neuroprotective, antidiabetic,
XX protozoacide, virucide, antibacterial and antiallergic activity.
XX Activation of signalling cascades through TNF family receptors,
XX especially induction of apoptosis and immunomodulation. The polypeptide
XX of the invention, also nucleic acid constructs, vectors and cells that
XX express them, are useful for treatment of cancers (solid or lymphatic
XX tumours), metabolic diseases, inflammation and autoimmune diseases,
XX particularly rheumatic/arthritic diseases, also multiple sclerosis,
XX diabetes mellitus, protozoal, bacterial and viral infections and
XX transplant rejection. The effect of the TNF family ligand is developed in
XX targeted, tissue- or cell-specific manner, so adverse systemic side
XX effects are avoided, or at least much reduced.
XX
XX Sequence 36 BP; 4 A; 14 C; 8 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 27; DB 12; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 42 CTCGCCATGTTCTGCTGCTCTGCAG 68
Db 10 CTCGCCATGTTCTGCTGCTCTGCAG 36
XX
XX RESULT 11
XX ADP20785/c
XX ID ADP20785 standard; DNA; 33 BP.
XX AC ADP20785;
XX
XX 12-AUG-2004 (first entry)
XX
XX CD40ex-Flag-TRAILex PCR primer 1161.
XX
XX ss; binding domain; cell-surface molecule; tumour necrosis factor;
XX TNF ligand family; TRAIL; TNF receptor superfamily; cytostatic;
XX antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
XX neuroprotective; antidiabetic; protozoacide; virucide; antibacterial;
XX antiallergic; signalling cascade; apoptosis; immunomodulation; cancer;
XX metabolic disease; multiple sclerosis; diabetes mellitus;
XX transplant rejection.
XX
XX Synthetic.
XX
XX OS
```

XX	Human; TRAF protein; Tumour-necrosis factor; TNF; CD40; PCR primer; ss;
KW	TNF receptor-associated factor; cell proliferation; cell differentiation; apoptosis; inflammation; immune response; receptor-ligand binding assay.
KW	
KW	
OS	Homo sapiens.
XX	
FN	WO200026670-A1.
XX	
PD	11-MAY-2000.
XX	
FF	23-AUG-1999; 99WO-US019272.
XX	
PR	29-OCT-1998; 98US-00181958.
XX	(BOEH) BOEHRINGER INGELHEIM PHARM INC.
PA	
FI	Kehry MR, Pullen SS, Crute JJ;
XX	WPI; 2000-451628/39.
DR	
XX	
PT	Quantitative assay for measuring the effect of a substance on tumor necrosis factor receptor associated factor protein interaction with it receptor.
FT	
XX	
PS	Example 1; Page 7; 27pp; English.
XX	
CC	Tumour necrosis factor (TNF) receptor has an important role in the regulation of cellular proliferation, differentiation, and apoptosis in inflammatory and immune responses. The present invention relates to a quantitative assay for measuring the ability of a substance to its binding of a TNF receptor-associated factor (TRAF) protein to its receptor. CD40 is a TRAF2 receptor. The present sequence is a PCR primer used to amplify amino acids 216 to 277 of human CD40 cytoplasmic domain (CD40c). Peptide antagonists of CD40c-TRAF2 binding were identified by the present invention (AAB07004 to AAB07010)
CC	
XX	
SQ	Sequence 37 BP; 12 A; 12 C; 11 G; 2 T; 0 U; 0 Other;
Query Match 2.6%; Score 26.4; DB 3; Length 37;	
Best Local Similarity 83.3%; Pred. No. 1.9e+03;	
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	681 CTGTCCTTTATCAAAAAGGTGGCCAAGAAGCACAACC 716 2 CGGCCCATGCACAAAGAAGTGGCCACGAGAGCCCAACC 37
DB	
RESULT 13	
ID	ADP12202/c
ID	ADP12202 standard; DNA; 26 BP.
XX	
AC	ADP12202;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Taqman probe set # 60.
XX	
KW	transplant rejection; immune system; rheumatoid arthritis; lupus;
KW	inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.
XX	
OS	Homo sapiens.
XX	
PN	WO2004042346-A2.
XX	
PD	21-MAY-2004.
XX	
PF	24-APR-2003; 2003WO-US012946.
XX	
PR	24-APR-2002; 2002US-00131831.
PR	20-DEC-2002; 2002US-00325899.
XX	
PA	(EXPR-) EXPRESSION DIAGNOSTICS INC.

DE10247755-A1.
 22-APR-2004.
 14-OCT-2002; 2002DE-01047755.
 14-OCT-2002; 2002DE-01047755.
 (PFIZ/) PFIZENMAIER K.
 (WAJA/) WAJANT H.
 Pfizermaier K, Wajant H;
 WPI; 2004-331870/31.
 New fusion polypeptide, useful for treating e.g. cancer, infections and inflammation, comprises binding domain for cell-surface molecule and fragment of tumor necrosis factor ligand.
 Example 1; Page 9; 16pp; German.
 This invention describes a novel polypeptide which comprises a segment that contains a binding domain for a cell-surface molecule; a peptide linker and a segment that contains a fragment of a member of the tumour necrosis factor (TNF) ligand (TRAIL) family that, alone, is inactive or has limited activity. The binding domain is not derived from an immunoglobulin and the TRAIL fragment becomes fully active only after binding of the binding domain to a cell-surface molecule. The TNF ligand fragment is the extracellular domain (or its functional variants or fragments) of a TNF family ligand, especially TRAIL, Fas, TNF, 41BBL, CD40L, CD30L or OX40L. The binding domain binds to a membrane protein and is at least the essential part of a ligand for a membrane-bound receptor, specifically where the ligand is a peptide or protein hormone (especially a growth factor, e.g. epidermal growth factor, or an angiogenic agent, e.g. vascular endothelial growth factor) or a cytokine. Alternatively, the binding domain is derived from a receptor, especially of the TNF receptor superfamily, e.g. TNF-R2, CD30, CD40 or CD28, for a membrane-bound ligand, provided that it does not bind to the extracellular domain of the ligand from which TNF ligand segment is derived. The products of the invention have cytostatic, antiinflammatory, immunosuppressive, antitumouric, antiarthritic, neuroprotective, antidiabetic, antiprotazoacide, virucide, antibacterial and antiallergic activity. Activation of signalling cascades through TNF family receptors, especially induction of apoptosis and immunomodulation. The polypeptide of the invention, also nucleic acid constructs, vectors and cells that express them, are useful for treatment of cancers (solid or lymphatic tumours), metabolic diseases, inflammation and autoimmune diseases, particularly rheumatic/arthritis diseases, and viral infections and diabetes mellitus, protozoal, bacterial and viral infections and transplant rejection. The effect of the TNF family ligand is developed in targeted, tissue- or cell-specific manner, so adverse systemic side effects are avoided, or at least much reduced.
 Sequence 33 BP; 7 A; 13 C; 10 G; 3 T; 0 U; 0 Other;
 Query Match 2.7%; Score 26.8; DB 12; Length 33;
 Best Local Similarity 93.3%; Pred. NO. 1.4e+03;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0
 QY 600 GTCTGTGGTCCCGAGGATCGGCTGAGAGCC 629
 |||||
 Db 33 GTCTGTGGTCCCGAGGATCGGCTGAGATCC 4
 RESULT 12
 AAA50913
 ID ID AAA50913 standard; DNA; 37 BP.
 XX AC AAA50913;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Human CD40 cytoplasmic domain PCR primer # 1.

```
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 58; SEQ ID NO 2211; 1762pp; English.
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC probe for a 50 mer oligonucleotide marker for diagnosis and monitoring of
CC allograft rejection and other disorders.
XX
XX Sequence 26 BP; 1 A; 6 C; 7 G; 12 T; 0 U; 0 Other;
SQ Query Match 2.6%; Score 26; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 692 CAAAAGGTGGCCCAAGGCAACCA 717
Db 26 CAAAAGGTGGCCCAAGGCAACCA 1
|||||
RESULT 14
AAZ40939
ID AAZ40939 standard; DNA; 25 BP.
XX
XX AAZ40939;
DT 26-JAN-2000 (first entry)
XX
DE Human CD40 PCR probe SEQ ID NO:88.
XX
XX Identification; genetic target; gene modulation; human; probe;
KW antisense oligonucleotide; phosphorothioate; PCR primer;
KW nucleotide sequence-based technology; antisense drug discovery;
KW target validation; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX W09953101-A1.
XX
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99WO-US008268.
XX
XX 13-APR-1998; 98US-0081483P.
XX
XX 28-APR-1998; 98US-00067638.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
XX WPI; 1999-620446/53.
XX
```

```
PT Identifying compounds which modulate expression of nucleic acids, used to
PT provide compounds having defined physical, chemical or bioactive
XX properties, e.g. antisense activity.
XX Example 10; Page 84; 264pp; English.
XX
XX A method has been developed of defining a set of compounds that modulate
CC the expression of a target nucleic acid (tNA) sequence via binding of the
CC compounds with the tNA sequence. The method comprises generating a
CC library of virtual compounds in silico according to defined criteria, and
CC evaluating in silico the binding of the virtual compounds with the tNA
CC according to defined criteria. Also described are: (1) a method of
CC defining a set of oligonucleotides (ONs) that modulate the expression of
CC a tNA sequence via binding of the ONs with the tNA sequence comprising
CC generating a library of virtual compounds in silico according to defined
CC criteria, and evaluating in silico the binding of the virtual ONs with
CC the tNA according to defined criteria; and (2) a method of defining a set
CC of compounds that modulate the expression of a tNA sequence via binding
CC of the compounds with the tNA. The methods can be used for the generation
CC and identification of synthetic compounds having defined physical,
CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC AAY52701 to AAY52706, represent sequences used in the exemplification of
CC the present invention.
XX
XX Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
SQ Query Match 2.5%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 226 TTCTTGGCGTGAAGCGAATTCCT 250
Db 1 TTCTTGGCGTGAAGCGAATTCCT 25
|||||
RESULT 15
AAZ47772
ID AAZ47772 standard; DNA; 25 BP.
XX
XX AAZ47772;
DT 02-MAR-2000 (first entry)
XX
DE Human CD40 PCR probe SEQ ID NO:88.
XX
XX Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
KW expression; immune disease; inflammatory disease; immunomodulatory;
KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;
KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour; PCR;
KW probe; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX W09957320-A1.
XX
XX 11-NOV-1999.
XX
XX 22-APR-1999; 99WO-US008765.
XX
XX 01-MAY-1998; 98US-00071433.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsert LM;
XX WPI; 2000-062158/05.
XX
```

PT Antisense molecules directed against nucleic acid encoding human CD40,
XX for treating e.g. immune, inflammatory or hyperproliferative diseases.
PS Example 14; Page 52; 102pp; English.
XX
CC AA247685 to AA247768 represent phosphorothioate antisense
CC oligonucleotides targeted to human CD40, which can be used to inhibit the
CC expression of human CD40. CD40 is involved in lymphocyte activation,
CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
CC prevent immune-associated diseases (specifically guest vs. host disease,
CC allograft rejection or autoimmune diseases); inflammation (specifically
CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
CC disease or psoriasis) or hyperproliferation (specifically cancer and
CC tumours). the antisense oligonucleotides are also useful as diagnostic
CC and research reagents. AA247769 represents the human CD40 nucleotide
CC sequence. AA247770 to AA247772 represent human CD40 forward and reverse
CC PCR primers, and a human CD40 PCR probe, respectively. AA247773 to
CC AA247775 represent other PCR primers and a probe used in the
CC exemplification of the present invention
XX
SQ Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 226 TTCCTTGGGTGAAGCGAATTCCT 250
Db 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 16
ADY75649
ID ADY75649 standard; DNA; 25 BP.
XX
AC ADY75649;
XX
DT 02-JUN-2005 (first entry)
DE Human CD40 RT-PCR probe.
XX
KW RT-PCR; probe; ss; diagnosis; drug discovery; mass spectroscopy;
KW reverse transcriptase PCR; CD40.
XX
OS Homo sapiens.
XX
PN WO2005023986-A2.
XX
PD 17-MAR-2005.
XX
PF 07-SEP-2004; 2004WO-US028879.
XX
PR 04-SEP-2003; 2003US-0500723P.
PR 04-SEP-2003; 2003US-0500724P.
PR 04-SEP-2003; 2003US-0500730P.
PR 04-SEP-2003; 2003US-0500732P.
PR 04-SEP-2003; 2003US-0500824P.
PR 11-SEP-2003; 2003US-0502007P.
PR 11-SEP-2003; 2003US-0502076P.
PR 17-SEP-2003; 2003US-0504495P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freier SM;
XX
DR WPI; 2005-233282/24.
XX
PT Selecting a target molecule having affinity for a ligand that is equal
PT to/greater than a baseline affinity by introducing a target molecule into
PT a ligand and standard target test mixture and identifying complex by mass
PT spectrometer.
XX
PS Example 65; SEQ ID NO 154; 314pp; English.

XX
CC The invention relates to selecting a target molecule that has an affinity
CC for a ligand that is equal to or greater than a baseline affinity,
CC comprises introducing a target molecule into a test mixture of the ligand
CC and a standard target, introducing the test mixture into a mass
CC spectrometer and identifying any complexes of the target molecule and the
CC ligand. Also included are a method of detecting a ligand-target complex
CC having an affinity as expressed as a dissociation constant of nanomolar-
CC 100 millimolar, a method for determining the relative interaction between
CC at least two molecules determining target a ligand, a method of
CC determining binding interaction (between a first target molecule and a
CC second target molecule with respect to a ligand), a method of determining
CC the relative proximity of binding sites for a first target molecule and a
CC second target molecule on a ligand, a method of determining the relative
CC orientation of a first target molecule to a second target molecule when
CC bound to a ligand, a method for screening target molecules having binding
CC affinity to a ligand, a method for modulating the binding affinity of a
CC target molecule for a ligand, a method for refining the binding of a
CC target molecule to a ligand, a method of favoring an alternate structure
CC of an oligomer, a method for identifying a ligand that alters a target
CC compound secondary structure, a method of determining the relative change
CC in proximity of binding sites for a first ligand and a second ligand on a
CC target substrate influenced by the first ligand, a method of determining
CC the relative change in proximity of a first binding site for a binding
CC ligand and a second binding site for a second binding ligand on a target,
CC a method of determining the relative orientation of a first ligand to a
CC second ligand when bound to a target substrate, an oligomeric compound
CC comprising a nucleotide sequence at least 80% complementary to a target
CC RNA (where the oligomeric compound comprises 21-24 nucleotides, and
CC comprises a nucleotide sequence that corresponds to a portion of the
CC nucleotide sequence of a larger oligomeric compound that comprises a
CC stemloop structure), a method of modulating transcription in a cell, a
CC method of modulating translation in a cell, a method of modulating a
CC conversion of a precursor RNA into a microRNA in a cell, a method of
CC generating a set of (oligomeric) compounds that modulate the expression
CC of a target nucleic acid molecule, a computer formatted medium comprising
CC computer readable instructions for identifying active compounds or for
CC performing the method above, a method of predicting evolutionarily
CC allowed mutations of a microRNA, a method of grouping biological members
CC according to a grouping criteria, a method of determining a blur-factor
CC and a method of determining a group of probable mutations for a microRNA.
CC The methods of the invention may be applied to the design of siRNA (short
CC interfering RNA) and antisense oligonucleotides. The method is useful for
CC determining the mode of binding interaction between two or more target
CC molecules to the ligand as well as their relative affinities. The
CC oligomeric compounds are useful in drug discovery and target validation,
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence is an RT-PCR (reverse transcriptase PCR) probe for
CC human CD40 mRNA used to assess expression of CD40 during treatment with
CC antisense oligonucleotides targeted to the human CD40 gene, designed
CC according to the methods of the invention.
XX
SQ Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 2.5%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 226 TTCCTTGGGTGAAGCGAATTCCT 250
Db 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 17
ADC79171
ID ADC79171 standard; DNA; 33 BP.
XX
AC ADC79171;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human CD40 forward PCR primer.
XX

KW ss; antigen-presenting vesicle; subcellular; T lymphocyte; anergisation;
 KW negative-regulatory T cell; cytostatic; immunostimulant; vaccine;
 KW viral-associated antigen; tumour-associated antigen; allergen;
 KW autoantigen; tumour; primer; PCR; human; CD40.
 XX
 OS Homo sapiens.
 XX
 XX EP1308167-A1.
 XX
 XX 07-MAY-2003.
 XX
 XX 06-NOV-2001; 2001EP-00126343.
 XX
 XX 06-NOV-2001; 2001EP-00126343.
 XX (PICKL) PICKL W.
 XX
 XX WPI; 2003-395754/38.
 XX
 XX New antigen-presenting vesicles, useful for treating, e.g. tumors,
 PT comprises surface molecules that signal antigen-specific activation or
 PT anergization of T cells.
 XX
 XX Example 1; SEQ ID NO 9; 28pp; German.
 XX
 CC This invention describes a novel antigen-presenting, preferably
 CC subcellular, vesicle comprising molecules on its surface for first, and
 CC preferably second, signals for antigen-specific activation of T
 CC lymphocytes or a first signal for antigen-specific anergisation of such
 CC cells or for induction of negative-regulatory T cells. The vesicles of
 CC the invention have cytostatic and immunostimulant activity and are used
 CC in vaccines, particularly where the HLA and peptide components are
 CC matched to a particular recipient or specific for a viral or tumour-
 CC associated antigen against which T cells are to be activated, or are from
 CC an allergen or autoantigen against which energy is required. Particularly
 CC the vesicles are used to treat, or screen, tumours, to induce an immune
 CC response to a weak antigen, for analysis of new costimulatory, adhesion
 CC or other molecules, for controlled release of messengers and/or growth
 CC factors contained within its lumen and as a platform for preparing
 CC multivalent binding reagents, e.g. for antigen-specific characterisation
 CC of animals. This sequence represents a primer used to generate the
 CC vesicles of the invention.
 XX
 SQ Sequence 33 BP; 7 A; 13 C; 10 G; 3 T; 0 U; 0 Other;
 Query Match 2.5%; Score 25; DB 10; Length 33;
 Best Local Similarity 84.8%; Pred. No. 4.7e+03;
 Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 95 CGCTGTCCATCCAGAACCCACTGCGATGCAG 127
 DB 1 CGCGGGGATCCGAAACCAACCCACTGCGATGCAG 33
 RESULT 18
 AAD03093/c
 ID AAD03093 standard; DNA; 50 BP.
 AC AAD03093;
 XX
 XX 13-JUN-2001 (first entry)
 XX
 XX 1467-05 oligonucleotide, to generate human met-Fc-OPG fusion construct.
 DE
 XX Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
 KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
 KW periodontal; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200118203-A1.
 PN

XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-US022797.
 PF
 XX 03-SEP-1999; 99US-00389782.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Dunstan CR, Wooden SK, Mann MB;
 PI
 XX WPI; 2001-244572/25.
 DR
 XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
 PT by e.g. osteoporosis, Paget's disease and osteomyelitis.
 XX
 XX Example 1; Page 47; 119pp; English.
 PS
 XX The patent discloses fusion protein comprising human osteoprotegerin
 CC (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively
 CC regulates formation of osteoclasts in vitro and in vivo. It blocks the
 CC differentiation of osteoclasts from monocyte or macrophage precursors and
 CC the reabsorption of bone. The OPG-Fc fusion protein are administered for
 CC the treatment of bone loss resulting from osteoporosis, Paget's disease,
 CC osteomyelitis, hypercalcaemia, osteopenia associated with surgery or
 CC steroid administration, osteonecrosis, bone loss due to rheumatoid
 CC arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic
 CC loosening. The present DNA sequence is 1467-05 oligonucleotide which is
 CC used to generate human met-Fc (lacking 1-5 residues)-OPG (22-194
 CC residues) fusion construct
 XX
 SQ Sequence 50 BP; 12 A; 10 C; 17 G; 11 T; 0 U; 0 Other;
 Query Match 2.5%; Score 25; DB 4; Length 50;
 Best Local Similarity 69.4%; Pred. No. 5.7e+03;
 Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 466 ATACCATCTGCGAGCCCTGCCAGTCGGCTTCTTCCCAATGTCATC 514
 DB 50 ACACCGTTTGCACAAAGTTGCCGACGGTTCTTCTTCCACGAACCTC 2
 RESULT 19
 ADO26914/c
 ID ADO26914 standard; DNA; 35 BP.
 XX
 AC ADO26914;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 XX CD40 transmembrane & cytoplasmic domain PCR primer #2.
 XX
 XX CD40 transmembrane domain; CD40 cytoplasmic domain; CD40; CD40t/c; PCR;
 KW primer; ss.
 XX
 OS Synthetic.
 XX
 XX GB2395554-A.
 PN
 XX 26-MAY-2004.
 XX
 XX 19-NOV-2002; 2002GB-00026909.
 PF
 XX 19-NOV-2002; 2002GB-00026909.
 PR
 XX (ALLI-) ALLIGATOR BIOSCIENCE AB.
 PA
 XX Ellmark P, Furebring C, Ohlin M, Borrebaeck CAK;
 PI
 XX WPI; 2004-422835/40.
 DR
 XX Identifying members of specific binding pairs in cell expressing first
 PT binding pair member (PBM) fused to apoptosis inhibitor by identifying

PT	inhibition of apoptosis caused by binding of FBM to second binding pair member.
XX	
PS	Example 1; Page 32; 84pp; English.
XX	
CC	The present invention relates to a method for identifying members of specific binding pairs. The method comprises providing a cell which is susceptible to apoptosis, expressing in the cell a first binding pair member (FBM) fused to apoptosis inhibitor, exposing the cell to an CC apoptosis inducing agent and contacting the cell with a second binding pair member (SBM), where members of specific binding pairs are identified by binding of FBM to SBM, such that apoptosis inhibitor is activated to CC inhibit apoptosis. The method is useful for screening human cDNA libraries for target antigens e.g., tumour epitopes. Preferably, the FBM CC are expressed as fusion proteins with the signalling portion (the CC transmembrane and cytoplasmic) of CD40 (CD40t/c). The present sequence is CC a PCR primer used in an example from the invention.
XX	
SQ	Sequence 35 BP; 6 A; 13 C; 8 G; 8 T; 0 U; 0 Other;
	Query Match 2.5%; Score 24.6; DB 12; Length 35;
	Best Local Similarity 87.1%; Pred. No. 6.3e+03;
	Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	859 TTCAGTGTGAGGAGACAGTCAGTGCGCAC 889 Db 35 TTCAGTGTGAGGAGACAGTCAGTGCGCAGC 5
RESULT 20	
ADO26923/c	ID
XX	ADO26923 standard; DNA; 35 BP.
AC	ADO26923;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	CD40 variant PCR primer G.
XX	
KW	CD40 transmembrane domain; CD40 cytoplasmic domain; CD40; CD40t/c; PCR;
KW	primer; ss.
OS	Synthetic.
XX	
PN	GB2395554-A.
XX	
PD	26-MAY-2004.
XX	
PF	19-NOV-2002; 2002GB-00026909.
PR	
PR	19-NOV-2002; 2002GB-00026909.
XX	
PA	(ALLI-) ALLIGATOR BIOSCIENCE AB.
XX	
PI	Ellmark P, Furebring C, Ohlin M, Borrebaeck CAK;
XX	
DR	WPI; 2004-422835/40.
XX	
PT	Identifying members of specific binding pairs in cell expressing first binding pair member (FBM) fused to apoptosis inhibitor by identifying inhibition of apoptosis caused by binding of FBM to second binding pair member.
XX	
PS	Example 2; Page 51; 84pp; English.
XX	
CC	The present invention relates to a method for identifying members of specific binding pairs. The method comprises providing a cell which is susceptible to apoptosis, expressing in the cell a first binding pair member (FBM) fused to apoptosis inhibitor, exposing the cell to an CC apoptosis inducing agent and contacting the cell with a second binding pair member (SBM), where members of specific binding pairs are identified by binding of FBM to SBM, such that apoptosis inhibitor is activated to CC inhibit apoptosis. The method is useful for screening human cDNA

```

CC libraries for target antigens e.g., tumour epitopes. Preferably, the FBM
CC are expressed as fusion proteins with the signalling portion (the
CC transmembrane and cytoplasmic) of CD40 (CD40t/c). The present sequence is
CC a PCR primer used in an example from the invention.
XX
XX
SQ Sequence 35 BP; 6 A; 13 C; 8 G; 8 T; 0 U; 0 Other;

Query Match      2.5%; Score 24.6; DB 12; Length 35;
Best Local Similarity 87.1%; Pred. No. 6.3e+03;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY      859  TCTCAGTGCAGGAGAGACAGTGCAGGCTGCAC 889
      |||||
DB       35  TCTCAGTGCAGGAGAGACAGTGCAGTGCAGCGC 5

RESULT 21
AAA51858
ID AAA51858 standard; DNA; 24 BP.
XX
XX AAA51858;
XX
XX 31-OCT-2000 (first entry)
XX
XX Primer A for porcine CD40 cDNA amplification.
XX
XX CD40 antigen; xenograft; CD40-deficient donor; graft rejection;
KW transgenic pig; reduced immunogenicity; immunosuppressive; gene therapy;
KW primer; ss.
XX
XX Homo sapiens.
OS
OS Mus sp.
OS Bos taurus.
XX
XX WO200039294-A1.
XX
XX 06-JUL-2000.
XX
XX 22-DEC-1999; 99WO-EP010332.
XX
XX 24-DEC-1998; 98GB-00028705.
XX 10-FEB-1999; 99GB-00002940.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Bravery C, Rushworth S, Thompson S;
XX WPI; 2000-452392/39.
XX
XX Ameliorating cellular graft rejection in a recipient mammal using CD40-
PT deficient donor mammal cells, tissues or organs as a xenograft, comprises
PT inactivation of the CD40 antigen gene with a targeting vector.

```

CC libraries for target antigens e.g., tumour epitopes. Preferably, the FBM
CC are expressed as fusion proteins with the signalling portion (the
CC transmembrane and cytoplasmic) of CD40 (CD40t/c). The present sequence is
CC a PCR primer used in an example from the invention.

XX
XX
SQ Sequence 35 BP; 6 A; 13 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 2.5%; Score 24.6; DB 12; Length 35;
Best Local Similarity 87.1%; Pred. No. 6.3e+03;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 859 TCTCAGTCGAGGAGACAGTCAGTCGCGTCAC 889
|||
Dd 35 TCTCAGTCGAGGAGAGACAGTCAGTCGACGC 5

RESULT 21
AAA51858
ID ID AAA51858 standard; DNA; 24 BP.
XX AC
XX AAA51858;
XX AC
XX
DT 31-OCT-2000 (first entry)
XX
XX Primer A for porcine CD40 cDNA amplification.
DE
XX
KW CD40 antigen; xenograft; CD40-deficient donor; graft rejection;
KW transgenic pig; reduced immunogenicity; immunosuppressive; gene therapy;
KW primer; ss.
XX
OS Homo sapiens.
OS Mus sp.
OS Bos taurus.
XX
PN W0200039294-A1.
XX
XX
PD 06-JUL-2000.
XX
XX 22-DEC-1999; 99WO-EP010332.
XX
XX 24-DEC-1998; 98GB-00028705.
PR 10-FEB-1999; 99GB-00002940.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Bravery C, Rushworth S, Thompson S;
PI
XX
XX WPI; 2000-452392/39.
XX
XX
XX Ameliorating cellular graft rejection in a recipient mammal using CD40-
PT deficient donor mammal cells, tissues or organs as a xenograft, comprises
PT inactivation of the CD40 antigen gene with a targeting vector.
XX
XX
XX Example 1; Page 8; 23pp; English.

CC Primers shown in AAA51858-59 were designed based on areas of sequence
CC conserved in the human, mouse and bovine CD40 genes. A fusion protein
CC consisting of the extracellular domain of human CD154 coupled to mouse Ig
CC kappa light chain was able to bind to porcine CD40, indicating that
CC direct signalling between a porcine graft and the immune cells of a human
CC host is possible through this molecular pathway. CD40-deficient donor
CC mammal cells, tissues or organs may be used for xenografting in order to
CC ameliorate cellular graft rejection in the recipient mammal. In
CC particular, porcine cells, tissues or organs are genetically modified so
CC that the cell surface expression of CD40 antigen is reduced. Transgenic
CC pigs may have an inactivated CD40 antigen gene and a transgene, e.g.
CC human Decay Accelerating Factor (hDAF) gene. The CD40-deficient donor
CC mammal cells, tissues or organs may be used as transplants (e.g. lung,
CC heart) in humans or other mammals (claimed). The transplants have a
CC reduced immunogenicity because the CD40 antigen gene is inactivated
XX
XX Sequence 24 BP; 3 A; 7 C; 4 G; 10 T; 0 U; 0 Other;

```
Query Match      2.4%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 TCGGCTTCTCTCCCAATGTGTCAT 513
Db 1 TCGGCTTCTCTCCCAATGTGTCAT 24

RESULT 22
ABN80809
ID ABN80809 standard; DNA; 24 BP.
AC ABN80809;
XX
XX
DT 15-JUL-2002 (first entry)
DE Human CD40 PCR primer SEQ ID NO 27.
XX
KW Human; IRF-1; transcription factor; interferon regulatory factor;
KW antisense; gene therapy; cardiovascular; transplant rejection;
KW immunological hypersensitivity; asthma; inflammatory disease; psoriasis;
KW Crohn's disease; autoimmune disease; diabetes mellitus; Th2 response;
KW multiple sclerosis; rheumatoid arthritis; Th1 response; Th2 response;
KW vasotrophic; immunosuppressive; antiasthmatic; dermatological;
KW antiallergic; antiulcer; antiinflammatory; antipsoriatic; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; PCR; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200229044-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-DE003835.
XX
XX 06-OCT-2000; 2000DE-01049549.
XX
XX 29-NOV-2000; 2000DE-01059144.
XX
XX (HECKER) HECKER M.
XX (WAGN) WAGNER A H.
XX
XX Hecker M, Wagner AH;
XX
XX WPI; 2002-383335/41.
XX
XX Inhibitor of the transcription factor IRF-1, useful for treating e.g.
XX transplant rejection and autoimmune disease, reduces expression of CD40.
XX
XX Example 2; Page 18; 45pp; German.
XX
XX The invention relates to an inhibitor (I) of the expression and/or
XX activity of the transcription factor (IRF-1; interferon regulatory
XX factor) as a therapeutic agent, especially an oligonucleotide inhibitor
XX (ABN80783-ABN80804) or antisense oligonucleotide (ABN80805-ABN80808) used
XX in antisense gene therapy. (I) are used to prevent or treat
XX cardiovascular complications such as restenosis after angioplasty or
XX stenosis of venous by-passes, chronic or acute transplant rejection and
XX graft versus host disease, immunological hypersensitivity, e.g. bronchial
XX asthma or atopic dermatitis, inflammatory diseases such as ulcerative
XX colitis, psoriasis and Crohn's disease and autoimmune diseases such as
XX diabetes mellitus, multiple sclerosis, collagenosis (e.g. systemic lupus
XX erythematosus), rheumatoid arthritis and vasculitis. (I) simultaneously
XX weaken both Th1 and Th2 responses. The present sequence is that of a PCR
XX primer, useful to the invention
XX
XX Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 373 GGCACGTGTACGAGTGAGGCTGTG 396
Db 1 GGCACGTGTACGAGTGAGGCTGTG 24

RESULT 24
ADD01329
ID ADD01329 standard; DNA; 24 BP.
XX
XX ADD01329;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human CD40 PCR primer SEQ ID 44.
XX
```

ss; inhibitor; STAT-1; signal transducer and activator of transcription;
 KW cardiovascular; restenosis; percutaneous angioplasty; stenosis;
 KW graft versus host reaction; ischaemic injury; reperfusion injury;
 KW organ transplantation; immunological hypersensitivity; allergic rhinitis;
 KW food; urticaria; celiac disease; contact dermatitis;
 KW immune complex disease; allergic vasculitis; gout; osteitis; osteomyelitis;
 KW glomerulonephritis; arthritis; hepatitis; myocarditis;
 KW polyneuritis; bronchitis; endocarditis; pancreatitis; septic shock;
 KW nephritis; pericarditis; peritonitis; hepatitis; myocarditis;
 KW vasotropic; immunosuppressive; anti-allergic; antiinflammatory;
 KW dermatological; antiarthritic; neurotropic; antigout; osteopathic;
 KW hepatotropic; virucide; cardiant; antibacterial; human; CD40; PCR;
 KW primer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003030944-A2.
 XX
 PD 17-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-DE003748.
 XX
 XX 04-OCT-2001; 2001DE-01048886.
 XX
 PA (AVON-) AVONTEC GMBH.
 XX
 PI Hecker M, Wagner AH;
 XX
 XX WPI; 2003-381684/36.
 DR
 XX
 XX Use of inhibitor of STAT-1 activity, for treating or preventing e.g.
 PT cardiovascular complications, graft versus host reactions or
 PT immunological hypersensitivity.
 XX
 PS Disclosure; SEQ ID NO 44; 53pp; German.

This invention describes the novel use of an inhibitor of STAT-1 (signal transducer and activator of transcription) for prevention or treatment of cardiovascular complications and other diseases e.g. restenosis after percutaneous angioplasty or stenosis in venous by-passes; graft versus host reactions; ischaemic reperfusion injury in surgical operations or organ transplantation, immunological hypersensitivity reactions, especially allergic rhinitis, food and medicine allergies (particularly urticaria and celiac disease), contact dermatitis, immune complex diseases, especially alveolitis, arthritis, glomerulonephritis and allergic vasculitis, inflammatory cartilage and bone diseases (especially arthritis, gout, osteitis and osteomyelitis), polyneuritis, also (sub)acute infection-related, particularly post-infection, inflammatory conditions, particularly bronchitis, endocarditis, hepatitis, myocarditis, nephritis, pericarditis, peritonitis and pancreatitis, including septic shock. The inhibitor is a double-stranded (ds) DNA oligonucleotide which acts as a decoy, a single-stranded antisense oligonucleotide, an antisense expression vector or ds RNA-interference (RNAi) oligonucleotide. The products of the invention have vasotropic, immunosuppressive, anti-allergic, antiinflammatory, dermatological, antiarthritic, neurotropic, antigout, osteopathic, hepatotropic, virucide, cardiant and antibacterial activity. ADD01286-ADD01346 represent the STAT-1 decoy oligonucleotides used in the method of the invention.

Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 2.4%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 202 CAGAGTTCACGAAACGGAATGCC 225
 |||||
 Db 1 CAGAGTTCACGAAACGGAATGCC 24

RESULT 25
 ADC79532

ID ADC79532 standard; DNA; 24 BP.
 XX
 AC ADC79532;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human CD40 PCR primer SEQ ID 44.
 XX
 KW vasotropic; anti-allergic; neuroprotective; immunosuppressive;
 KW antiarthritic; antiinflammatory; dermatological; antiarthritic;
 KW antiasthmatic; antidiabetic; antipsoriatic; antibacterial; STAT-1;
 KW proinflammatory; leucocyte; endothelial cell; smooth muscle cell; CD40;
 KW E-selectin; inducible nitric oxide synthase; iNOS; interleukin-12;
 KW interferon-gamma; cardiovascular; restenosis; percutaneous angioplasty;
 KW transplant rejection; graft versus host disease; reperfusion;
 KW hypersensitivity reaction; autoimmune disease; diabetes mellitus;
 KW multiple sclerosis; rheumatoid arthritis; chronic inflammatory disease;
 KW arthritis; asthma; bronchitis; psoriasis; neurodermatitis;
 KW ulcerative colitis; Crohn's disease; primer; ss; PCR.
 XX
 OS Homo sapiens.
 XX
 XX WO2003031459-A2.
 XX
 XX 17-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-DE003747.
 PF
 XX 04-OCT-2001; 2001DE-01048828.
 PR
 XX (AVON-) AVONTEC GMBH.
 PA
 XX Hecker M, Wagner AH;
 PI
 XX WPI; 2003-363361/34.
 DR
 XX
 XX New decoy oligonucleotides, useful for treating and preventing e.g.
 PT cardiovascular complications or transplant rejection, by neutralization
 PT of STAT-1.
 XX
 XX Example 2; SEQ ID NO 44; 52pp; German.
 CC This invention describes novel decoy oligonucleotides which have
 CC vasotropic, anti-allergic, neuroprotective, immunosuppressive,
 CC antiarthritic, antiinflammatory, dermatological, antiarthritic,
 CC antiasthmatic, antidiabetic, antipsoriatic and antibacterial activity.
 CC The oligonucleotides neutralise or inhibit expression of STAT-1 and thus
 CC of a range of potentially proinflammatory gene products in leucocytes,
 CC endothelial and smooth muscle cells. Genes that have a STAT-1 binding
 CC site in their promoters include those for CD40, E-selectin, inducible
 CC nitric oxide synthase (NOS), interleukin-12 and interferon-gamma. Also
 CC the oligonucleotides of the invention may lift inhibition of gene
 CC expression where this is blocked by transcription factors, e.g. the gene
 CC for endothelial NOS which is down regulated by interferon-gamma. The
 CC decoy oligonucleotide and new antisense oligonucleotides, are used to
 CC treat or prevent cardiovascular complications, especially restenosis
 CC after percutaneous angioplasty and stenosis in venous by-passes,
 CC transplant rejection, graft versus host disease, ischaemic/reperfusion
 CC injuries of surgery, immunological hypersensitivity reactions (types I-
 CC V), autoimmune diseases (especially diabetes mellitus, multiple sclerosis
 CC and rheumatoid arthritis), all forms of (sub)acute or chronic
 CC inflammatory diseases, especially of the joints (arthritis), respiratory
 CC organs (bronchial asthma and chronic bronchitis), skin (psoriasis and
 CC neurodermatitis) or gastrointestinal tract (ulcerative colitis or Crohn's
 CC disease). ADC79489-ADC79549 represent the decoy oligonucleotides
 CC described in the disclosure of the invention.
 XX
 XX
 SQ Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 2.4%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
 Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 26

ACC00576/c
 ID ACC00576 standard; DNA; 24 BP.

XX ACC00576;

XX 23-JUN-2003 (first entry)

XX Human CD40 DNA amplifying antisense primer.

XX Kidney disease; transplantation; nephric tissue; nephrotropic;
 KW cystostatic; litholytic; antidiabetic; thrombolytic; CD40; PCR; primer;
 KW ss.

XX Homo sapiens.

XX WO2003022123-A2.

XX 20-MAR-2003.

XX 01-SEP-2002; 2002WO-IL000722.

XX 07-SEP-2001; 2001US-0317452P.

XX 10-APR-2002; 2002US-00118933.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Reisner V, Dekel B;

XX WPI; 2003-354496/33.

XX Treating kidney disease e.g. chronic nephritis comprises transplanting
 PT human or porcine nephric tissue graft transplantation at differentiation
 PT stage corresponding to specific period of gestation.

XX Example 1; Page 24; 54pp; English.

XX The invention relates to treating a kidney disease and involves
 CC transplanting a graft of human nephric tissue at a differentiation stage
 CC corresponding to 4-10 weeks of gestation or transplanting a graft of
 CC porcine nephric tissue at a differentiation stage corresponding to 3-6
 CC weeks of gestation. The method is used for treating kidney disease and
 CC for evaluating transplant suitability. The kidney disease includes acute
 CC kidney failure, acute nephritic syndrome, analgesic nephropathy,
 CC atherembolic renal disease, chronic kidney failure, chronic nephritis,
 CC congenital nephrotic disease, end-stage renal disease, Goodpasture's
 CC syndrome, IgM mesangial proliferative glomerulonephritis, interstitial
 CC nephritis, kidney cancer, kidney damage, kidney infection, kidney injury,
 CC kidney stones, lupus nephritis, membranoproliferative glomerulonephritis
 CC I, membranoproliferative glomerulonephritis II, membranous nephropathy,
 CC necrotizing glomerulonephritis, nephroblastoma, nephrocalcinosis,
 CC nephrogenic diabetes insipidus, IgA-mediated nephropathy, nephrosis,
 CC nephritic syndrome, polycystic kidney disease, post-streptococcal
 CC glomerulonephritis, reflux nephropathy, renal artery embolism, renal
 CC artery stenosis, renal papillary necrosis, renal tubular acidosis type I,
 CC renal tubular acidosis type II, renal underperfusion and renal vein
 CC thrombosis. Sequences ACC00575-76 represent PCR primers for amplifying
 CC the human CD40 DNA

XX Sequence 24 BP; 7 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 GCTACAGGGGTTTCTGATACATC 473

Db 24 GCTACAGGGGTTTCTGATACATC 1

RESULT 27

ADO57906
 ID ADO57906 standard; DNA; 24 BP.

XX ADO57906;

XX 15-JUL-2004 (first entry)

XX Human CD4U RT-PCR forward primer.

XX immunosuppressive; vasotropic; double-stranded oligonucleotide;
 KW transcription factor; AP-1; acute transplant rejection;
 KW chronic transplant rejection; graft-versus-host disease;
 KW ischaemic injury; reperfusion injury; surgery;
 KW gene transcription modulation; reverse transcriptase PCR; RT-PCR; primer;
 KW ss; human; CD4U.

XX Homo sapiens.

XX DE10240417-A1.

XX 11-MAR-2004.

XX 02-SEP-2002; 2002DE-01040417.

XX 02-SEP-2002; 2002DE-01040417.

XX (AVON-) AVONTEC GMBH.

XX Hecker M, Wagner AH;

XX WPI; 2004-228818/22.

XX New double-stranded oligonucleotides that bind specifically to the AP-1
 PT transcription factor, useful for treating e.g. transplant rejection or
 PT ischemic/reperfusion injury.

XX Disclosure; SEQ ID NO 37; 31pp; German.

XX The invention describes double-stranded (ds) DNA oligonucleotides (I) in
 CC which one strand (Ia) has any of 26 sequences (some degenerate), given in
 CC the specification, and the other strand is complementary to (Ia). Also
 CC described are the use of (a) ds oligonucleotides (II) that bind to the
 CC transcription factor AP-1 or (b) ds oligonucleotides (III) having any of
 CC 36 specified sequences (these include (i) for preparing a composition
 CC for treatment or prevention of (i) acute or chronic transplant rejection
 CC and graft-versus-host disease or (ii) ischaemic/reperfusion injury to
 CC organs during surgery. (I), and other known ds oligonucleotides that bind
 CC to the transcription factor AP-1, are used to treat or prevent (i) acute
 CC or chronic transplant rejection and graft-versus-host disease or (ii)
 CC ischaemic/reperfusion injury to organs during surgery. They are also used
 CC to modulate gene transcription in cells, especially endothelial and
 CC antigen-presenting cells, e.g. by ex vivo treatment of donor organs
 CC before transplantation. (I) become active immediately after entering a
 CC cell, i.e. more quickly than antisense or interfering oligonucleotides.
 CC This sequence represents a reverse transcription PCR primer used in the
 CC isolation of human CD4U, used in an assay to determine the effect of ds
 CC oligonucleotides on AP-1 binding specificity.

XX Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 12; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225

Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 28

RESULT 29
AAQ55229

XX PD 20-JAN-1994.
 XX XX
 XX PF 08-JUL-1993; 93WO-US006432.
 XX XX
 XX PR 09-JUL-1992; 92US-00910222.
 XX PR 09-FEB-1993; 93US-00015147.
 XX PR 28-MAY-1993; 93US-00070158.
 XX XX
 XX PA (CETU) CETUS ONCOLOGY CORP.
 XX XX
 XX PI De Boer M, Conroy LB;
 XX XX
 XX DR WPI; 1994-035055/04.
 XX XX
 XX PT Antibodies to membrane-associated antigens - used for treating transplant
 XX PT rejection, graft-versus-host disease, antibody-mediated disease and auto-
 XX PT immune disease.
 XX XX
 XX PS Disclosure; Fig 2; 113pp; English.
 XX XX
 XX CC Primers (AAQ55223-30) are used to amplify the human CD40 antigen and the
 XX CC human B7 DNA. The CD40 antigen is immunoreactive with an anti- CD40 Mab.
 XX CC The binding of the Mab to the CD40 antigen is located on the surface of a
 XX CC human B cell. The antibodies can be used to treat transplant rejection
 XX CC diseases as well as autoimmune infections. (Updated on 25-MAR-2003 to
 XX CC correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
 XX XX
 XX SQ Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;
 XX
 XX Query Match 2.4%; Score 24; DB 2; Length 32;
 XX Best Local Similarity 100.0%; Pred. No. 9e+03;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
 XX ||||||||||||||||||
 XX Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32
 XX
 XX RESULT 31
 XX AAQ96203
 XX ID AAQ96203 standard; DNA; 32 BP.
 XX AC AAQ96203;
 XX AC
 XX DT 26-MAR-1996 (first entry)
 XX DE Primer #3.
 XX XX
 XX KW Polymerase chain reaction; PCR; primer; amplify; B7; B-cell; T-cell;
 XX KW baculovirus vector; hybridoma; antibody; antigen; immunosuppressor;
 XX KW interleukin-2; IL-2; transplant rejection; graft vs host disease; GVHD;
 XX KW rheumatoid arthritis; therapy; CD28; ss.
 XX OS Synthetic.
 XX OS
 XX PN WO9522619-A1.
 XX XX
 XX PD 24-AUG-1995.
 XX PF 19-JAN-1995; 95WO-US0000897.
 XX PR 18-FEB-1994; 94US-00200716.
 XX XX
 XX PA (CETU) CETUS ONCOLOGY CORP.
 XX PI De Boer M, Conroy LB;
 XX XX
 XX DR WPI; 1995-302723/39.
 XX XX
 XX PT T cell anergy induction by coadmin. of anti-B7-antibody and
 XX PT immunosuppressive agent - used to prevent transplant rejection, and to
 XX PT treat graft vs host disease and rheumatoid arthritis.

XX PS Disclosure; p57; 77pp; English.
 XX XX
 XX CC The sequences represented by AAQ96201-Q96204 are used in the invention.
 XX CC The sequences represented by AAQ96197 and AAQ96198 are primers for the
 XX CC full length B7-1. This sequence is also used (along with AAQ96200) as a
 XX CC primer for soluble B7-1. This sequence corresponds to bases 307-324 of
 XX CC the full length B7 gene. B7 is a monomeric transmembrane glycoprotein
 XX CC that is expressed on activated B-cells, and is a ligand for the CD28
 XX CC receptor of T-cells. There are three ligands of B7 (B7-1, B7-2, and B7-
 XX CC 3). The sequence amplified by these primers is inserted into a
 XX CC baculovirus vector and used for the production of B7-1 specific
 XX CC antibodies using hybridoma techniques. The anti-B7-1 antibodies can then
 XX CC be included in a composition containing an immunosuppressive agent that
 XX CC inhibits the production of interleukin-2 (IL-2) by T-cells. This
 XX CC composition can be administered to patients and thereby used to prevent
 XX CC transplant rejection, and to treat graft vs host disease (GVHD) and
 XX CC rheumatoid arthritis. The advantage with using this composition is that
 XX CC it induces long-lasting T-cell anergy against an alloantigen
 XX XX
 XX SQ Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;
 XX
 XX Query Match 2.4%; Score 24; DB 2; Length 32;
 XX Best Local Similarity 100.0%; Pred. No. 9e+03;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
 XX ||||||||||||||||||
 XX Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32
 XX
 XX RESULT 32
 XX AAQ96201
 XX ID AAQ96201 standard; DNA; 32 BP.
 XX AC AAQ96201;
 XX AC
 XX DT 26-MAR-1996 (first entry)
 XX DE Primer #1.
 XX XX
 XX KW Polymerase chain reaction; PCR; primer; amplify; B7; B-cell; T-cell;
 XX KW baculovirus vector; hybridoma; antibody; antigen; immunosuppressor;
 XX KW interleukin-2; IL-2; transplant rejection; graft vs host disease; GVHD;
 XX KW rheumatoid arthritis; therapy; CD28; ss.
 XX OS Synthetic.
 XX OS
 XX PN WO9522619-A1.
 XX XX
 XX PD 24-AUG-1995.
 XX PF 19-JAN-1995; 95WO-US0000897.
 XX PR 18-FEB-1994; 94US-00200716.
 XX XX
 XX PA (CETU) CETUS ONCOLOGY CORP.
 XX PI De Boer M, Conroy LB;
 XX XX
 XX DR WPI; 1995-302723/39.
 XX XX
 XX PT T cell anergy induction by coadmin. of anti-B7-antibody and
 XX PT immunosuppressive agent - used to prevent transplant rejection, and to
 XX PT treat graft vs host disease and rheumatoid arthritis.
 XX PS Disclosure; p56; 77pp; English.
 XX XX
 XX CC The sequences represented by AAQ96201-Q96204 are used in the invention.
 XX CC The sequences represented by AAQ96197 and AAQ96198 are primers for the
 XX CC full length B7-1. This sequence is also used (along with AAQ96200) as a
 XX CC primer for soluble B7-1. This sequence corresponds to bases 307-324 of
 XX CC the full length B7 gene. B7 is a monomeric transmembrane glycoprotein

CC that is expressed on activated B-cells, and is a ligand for the CD28
 CC receptor of T-cells. There are three ligands of B7 (B7-1, B7-2, and B7-
 CC 3). The sequence amplified by these primers is inserted into a
 CC baculovirus vector and used for the production of B7-1 specific
 CC antibodies using hybridoma techniques. The anti-B7-1 antibodies can then
 CC be included in a composition containing an immunosuppressive agent that
 CC inhibits the production of interleukin-2 (IL-2) by T-cells. This
 CC composition can be administered to patients and thereby used to prevent
 CC transplant rejection, and to treat graft vs host disease (GVHD) and
 CC rheumatoid arthritis. The advantage with using this composition is that
 CC it induces long-lasting T-cell anergy against an alloantigen
 XX
 SQ Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
 |||||
 Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 33
 AAT79188
 ID AAT79188 standard; DNA; 32 BP.

XX
 AC AAT79188;

DT 23-MAR-1998 (first entry)

DE Human soluble CD40 antigen PCR primer.

XX Human; B7 antigen; CD40; PCR primer; monoclonal antibody; B cell; growth;
 KW differentiation; allergy; autoimmune disease; ss.

OS Synthetic.

XX WO9731025-A1.

PD 28-AUG-1997.

PF 21-FEB-1997; 97WO-US002858.

XX 23-FEB-1996; 96US-00606293.

PA (CHIR) CHIRON CORP.

XX De Boer M;

XX WPI; 1997-435094/40.

XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
 PT prevent their growth and differentiation, useful to treat or prevent
 PT antibody mediated allergies and autoimmune diseases.

XX Example 1; Fig 2; 64pp; English.

XX A novel humanised monoclonal antibody (MAB) has been developed which: (a)
 CC binds a human CD40 antigen on the surface of a B cell, to prevent its
 CC growth and differentiation; and (b) has an effective number of exposed
 CC amino acids in its framework regions that are consistent with amino acid
 CC residues found in the corresponding framework regions of a human Ab to
 CC provide a reduced immunogenicity in humans. The present sequence
 CC represent a PCR primer used in an example of the present invention. The
 CC MAB can be used to prevent or treat antibody mediated diseases,
 CC particularly immunoglobulin E (IgE) mediated allergies, systemic lupus
 CC erythematosus, primary biliary cirrhosis, idiopathic thrombocytopenia
 CC purpura and rheumatoid arthritis. The MAB inhibits the normal B cell
 CC response to CD40 ligands at relatively low concentrations and is unlikely
 CC to cause any immune response in humans

XX Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
 |||||
 Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 34

AAT79186

ID AAT79186 standard; DNA; 32 BP.

XX AAT79186;

DT 23-MAR-1998 (first entry)

XX Human full length CD40 antigen PCR primer.

XX Human; B7 antigen; CD40; PCR primer; monoclonal antibody; B cell; growth;
 KW differentiation; allergy; autoimmune disease; ss.

OS Synthetic.

XX WO9731025-A1.

PD 28-AUG-1997.

PF 21-FEB-1997; 97WO-US002858.

XX 23-FEB-1996; 96US-00606293.

XX (CHIR) CHIRON CORP.

XX De Boer M;

XX WPI; 1997-435094/40.

XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
 PT prevent their growth and differentiation, useful to treat or prevent
 PT antibody mediated allergies and autoimmune diseases.

XX Example 1; Fig 2; 64pp; English.

XX A novel humanised monoclonal antibody (MAB) has been developed which: (a)
 CC binds a human CD40 antigen on the surface of a B cell, to prevent its
 CC growth and differentiation; and (b) has an effective number of exposed
 CC amino acids in its framework regions that are consistent with amino acid
 CC residues found in the corresponding framework regions of a human Ab to
 CC provide a reduced immunogenicity in humans. The present sequence
 CC represent a PCR primer used in an example of the present invention. The
 CC MAB can be used to prevent or treat antibody mediated diseases,
 CC particularly immunoglobulin E (IgE) mediated allergies, systemic lupus
 CC erythematosus, primary biliary cirrhosis, idiopathic thrombocytopenia
 CC purpura and rheumatoid arthritis. The MAB inhibits the normal B cell
 CC response to CD40 ligands at relatively low concentrations and is unlikely
 CC to cause any immune response in humans

XX Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
 |||||
 Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 35

AAQ55228/c

ID AAQ55228 standard; DNA; 34 BP.

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XX AC AAQ55228;
XX DT 25-MAR-2003 (revised)
XX DT 15-JUL-1994 (first entry)
XX DE Full length CD40 backward primer (MR112).
XX KW Antibody; monoclonal; membrane; transplant; rejection; sera; antigen;
XX KW graft-versus-host disease; auto-immune disease; allergy; cirrhosis;
XX KW idiopathic thrombocytopenic purpura; ss.
XX OS Synthetic.
XX PN WO9401547-A2.
XX PD 20-JAN-1994.
XX PF 08-JUL-1993; 93WO-US006432.
XX PR 09-JUL-1992; 92US-00910222.
XX PR 09-FEB-1993; 93US-00015147.
XX PR 28-MAY-1993; 93US-00070158.
XX PA (CETU ) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX PI WPI; 1994-035055/04.
XX DR Antibodies to membrane-associated antigens - used for treating transplant
XX PT rejection, graft-versus-host disease, antibody-mediated disease and auto-
XX PT immune disease.
XX PS Disclosure; Fig 2; 113pp; English.
XX CC Primers (AAQ55223-30) are used to amplify the human CD40 antigen and the
XX CC human B7 DNA. The CD40 antigen is immunoreactive with an anti- CD40 Mab.
XX CC The binding of the Mab to the CD40 antigen is located on the surface of a
XX CC human B cell. The antibodies can be used to treat transplant rejection
XX CC diseases as well as autoimmune infections. (Updated on 25-MAR-2003 to
XX CC correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 34 BP; 4 A; 12 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGTGG 905
DB 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 36
AAQ96202/c
ID AAQ96202 standard; DNA; 34 BP.
AC AAQ96202;
XX XX
XX DT 26-MAR-1996 (first entry)
XX DE Primer #2.
XX KW Polymerase chain reaction; PCR; primer; amplify; B7; B-cell; T-cell;
XX KW baculovirus vector; hybridoma; antibody; antigen; immunosuppressor;
XX KW interleukin-2; IL-2; transplant rejection; graft vs host disease; GVHD;
XX KW rheumatoid arthritis; therapy; CD28; ss.
XX OS Synthetic.
XX PN WO9522619-A1.
XX PI De Boer M;
XX PI

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PD XX 24-AUG-1995.
XX PF 19-JAN-1995; 95WO-US000897.
XX PR 18-FEB-1994; 94US-00200716.
XX PA (CETU ) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX PI WPI; 1995-302723/39.
XX DR T cell energy induction by coadmin. of anti-B7-antibody and
XX PT immunosuppressive agent - used to prevent transplant rejection, and to
XX PT treat graft vs host disease and rheumatoid arthritis.
XX PS Disclosure; p56; 77pp; English.
XX CC The sequences represented by AAQ96201-Q96204 are used in the invention.
XX CC The sequences represented by AAQ96197 and AAQ96198 are primers for the
XX CC full length B7-1. This sequence is also used (along with AAQ96200) as a
XX CC primer for soluble B7-1. This sequence corresponds to bases 307-324 of
XX CC the full length B7 gene. B7 is a monomeric transmembrane glycoprotein
XX CC that is expressed on activated B-cells, and is a ligand for the CD28
XX CC receptor of T-cells. There are three ligands of B7 (B7-1, B7-2, and B7-
XX CC 3). The sequence amplified by these primers is inserted into a
XX CC baculovirus vector and used for the production of B7-1 specific
XX CC antibodies using hybridoma techniques. The anti-B7-1 antibodies can then
XX CC be included in a composition containing an immunosuppressive agent that
XX CC inhibits the production of interleukin-2 (IL-2) by T-cells. This
XX CC composition can be administered to patients and thereby used to prevent
XX CC transplant rejection, and to treat graft vs host disease (GVHD) and
XX CC rheumatoid arthritis. The advantage with using this composition is that
XX CC it induces long-lasting T-cell anergy against an alloantigen
XX SQ Sequence 34 BP; 4 A; 12 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGTGG 905
DB 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 37
AAAT79187/c
ID AAAT79187 standard; DNA; 34 BP.
AC AAAT79187;
XX XX
XX DT 23-MAR-1998 (first entry)
XX DE Human full length CD40 antigen PCR primer.
XX KW Human; B7 antigen; CD40; PCR primer; monoclonal antibody; B cell; growth;
XX KW differentiation; allergy; autoimmune disease; ss.
XX OS Synthetic.
XX PN WO9731025-A1.
XX PD 28-AUG-1997.
XX PF 21-FEB-1997; 97WO-US002858.
XX PR 23-FEB-1996; 96US-00606293.
XX PA (CHIR ) CHIRON CORP.
XX PI De Boer M;
XX PI

```

DR WPI; 1997-435094/40.
 XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
 PT prevent their growth and differentiation, useful to treat or prevent
 PT antibody mediated allergies and autoimmune diseases.
 XX
 PS Example 1; Fig 2; 64pp; English.
 XX
 CC A novel humanised monoclonal antibody (MAb) has been developed which: (a)
 CC binds a human CD40 antigen on the surface of a B cell, to prevent its
 CC growth and differentiation; and (b) has an effective number of exposed
 CC amino acids in its framework regions that are consistent with amino acid
 CC residues found in the corresponding framework regions of a human Ab to
 CC provide a reduced immunogenicity in humans. The present sequence
 CC represent a PCR primer used in an example of the present invention. The
 CC MAb can be used to prevent or treat antibody mediated diseases,
 CC particularly immunoglobulin E (IgE) mediated allergies, systemic lupus
 CC erythematosus, primary biliary cirrhosis, idiopathic thrombocytopenia
 CC purpura and rheumatoid arthritis. The MAb inhibits the normal B cell
 CC response to CD40 ligands at relatively low concentrations and is unlikely
 CC to cause any immune response in humans
 XX
 SQ Sequence 34 BP; 4 A; 12 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 2.4%; Score 24; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 9.3e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 882 GGCTGCACCCACCCAGGAGTGTGG 905
 Db 34 GGCTGCACCCACCCAGGAGTGTGG 11
 RESULT 38
 ADE28512
 ID ADE28512 standard; DNA; 36 BP.
 XX
 AC ADE28512;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE PCR primer SEQ ID 135 used to amplify human CD40 extracellular cDNA.
 XX
 KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; PCR; primer; ss; extracellular domain.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040170-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 08-NOV-2002; 2002WO-US036107.
 XX
 PR 09-NOV-2001; 2001US-0348980P.
 XX
 PA (PFIZ) PFIZER PROD INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 XX
 DR WPI; 2003-441521/41.
 XX
 CC New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.
 XX
 PS Example 14; SEQ ID NO 135; 177pp; English.
 XX
 CC The invention relates to a novel chimeric or human monoclonal antibody or

CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody-related PCR primer of the invention.
 XX
 SQ Sequence 36 BP; 6 A; 11 C; 9 G; 10 T; 0 U; 0 Other;
 Query Match 2.3%; Score 23.4; DB 10; Length 36;
 Best Local Similarity 96.0%; Pred. No. 1.4e+04;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 46 CCATGGTTCGCTGCTCTGCAGTG 70
 Db 12 CAATGGTTCGCTGCTCTGCAGTG 36
 RESULT 39
 AAZ40937
 ID AAZ40937 standard; DNA; 23 BP.
 XX
 AC AAZ40937;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE Human CD40 PCR forward primer SEQ ID NO:86.
 XX
 KW Identification; genetic target; gene modulation; human; probe;
 KW antisense oligonucleotide; phosphorothioate; PCR primer;
 KW nucleotide sequence-based technology; antisense drug discovery;
 KW target validation; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9953101-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 13-APR-1999; 99WO-US008268.
 XX
 PR 13-APR-1998; 98US-0081483P.
 PR 28-APR-1998; 98US-00067638.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Cowser LM, Baker BF, McNeill J, Freier SM, Saamur HM, Brooks DG;
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
 XX
 DR WPI; 1999-620446/53.
 XX
 CC Identifying compounds which modulate expression of nucleic acids, used to
 PT provide compounds having defined physical, chemical or bioactive
 PT properties, e.g. antisense activity.
 XX
 PS Example 10; Page 84; 264pp; English.
 XX
 CC A method has been developed of defining a set of compounds that modulate
 CC the expression of a target nucleic acid (tNA) sequence via binding of the
 CC compounds with the tNA sequence. The method comprises generating a
 CC library of virtual compounds in silico according to defined criteria, and
 CC evaluating in silico the binding of the virtual compounds with the tNA
 CC according to defined criteria. Also described are: (1) a method of
 CC defining a set of oligonucleotides (ONs) that modulate the expression of
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising
 CC generating a library of virtual compounds in silico according to defined
 CC criteria, and evaluating in silico the binding of the virtual ONs with
 CC the tNA according to defined criteria; and (2) a method of defining a set

CC of compounds that modulate the expression of a tNA sequence via binding
CC and identification of synthetic compounds having defined physical,
CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC AAY52701 to AAY52706, represent sequences used in the exemplification of
CC the present invention

XX SQ Sequence 23 BP; 8 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACGAAACGGAATGC 224
|||||
Db 1 CAGAGTTCACGAAACGGAATGC 23

RESULT 40
AAZ40938/c
ID AAZ40938 standard; DNA; 23 BP.

XX AC AAZ40938;

XX DT 26-JAN-2000 (first entry)

XX DE Human CD40 PCR reverse primer SEQ ID NO:87.

XX KW Identification; genetic target; gene modulation; human; probe;
XX antisense oligonucleotide; phosphorothioate; PCR primer;
XX nucleotide sequence-based technology; antisense drug discovery;
XX target validation; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09953101-A1.

XX PD 21-OCT-1999.

XX PF 13-APR-1999; 99WO-US008268.

XX PR 13-APR-1998; 98US-0081483P.

XX PR 28-APR-1998; 98US-00067638.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Cowser LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;

XX PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;

XX DR WPI; 1999-620446/53.

XX PT Identifying compounds which modulate expression of nucleic acids, used to
XX provide compounds having defined physical, chemical or bioactive
XX properties, e.g. antisense activity.

XX PS Example 10; Page 84; 264pp; English.

XX CC A method has been developed of defining a set of compounds that modulate
XX the expression of a target nucleic acid (tNA) sequence via binding of the
XX compounds with the tNA sequence. The method comprises generating a
XX library of virtual compounds in silico according to defined criteria, and
XX evaluating in silico the binding of the virtual compounds with the tNA
XX according to defined criteria. Also described are: (1) a method of
XX defining a set of oligonucleotides (ONs) that modulate the expression of
XX a tNA sequence via binding of the ONs with the tNA sequence comprising
XX generating a library of virtual compounds in silico according to defined
XX criteria, and evaluating in silico the binding of the virtual ONs with
XX the tNA according to defined criteria; and (2) a method of defining a set
XX of compounds that modulate the expression of a tNA sequence via binding

CC of the compounds with the tNA. The methods can be used for the generation
CC and identification of synthetic compounds having defined physical,
CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC AAY52701 to AAY52706, represent sequences used in the exemplification of
CC the present invention

XX SQ Sequence 23 BP; 1 A; 5 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GAACAGAGAGACACACTGCCACC 282
|||||
Db 23 GAACAGAGAGACACACTGCCACC 1

RESULT 41

AAZ47771/c

ID AAZ47771 standard; DNA; 23 BP.

XX AC AAZ47771;

XX DT 02-MAR-2000 (first entry)

XX DE Human CD40 reverse PCR primer SEQ ID NO:87.

XX KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
XX expression; immune disease; inflammatory disease; immunomodulatory;
XX anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
XX anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;
XX hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
XX inflammatory bowel disease; asthma; psoriasis; cancer; tumour;
XX PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09957320-A1.

XX PD 11-NOV-1999.

XX PF 22-APR-1999; 99WO-US008765.

XX PR 01-MAY-1998; 98US-00071433.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Cowser LM;

XX DR WPI; 2000-062158/05.

XX PT Antisense molecules directed against nucleic acid encoding human CD40,
XX for treating e.g. immune, inflammatory or hyperproliferative diseases.

XX PS Example 13; Page 50; 102pp; English.

XX CC AAZ47685 to AAZ47768 represent phosphorothioate antisense
XX oligonucleotides targeted to human CD40, which can be used to inhibit the
XX expression of human CD40. CD40 is involved in lymphocyte activation,
XX tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
XX prevent immune-associated diseases (specifically guest vs. host disease,
XX allograft rejection or autoimmune diseases); inflammation (specifically
XX asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
XX disease or psoriasis) or hyperproliferation (specifically cancer and
XX tumours). the antisense oligonucleotides are also useful as diagnostic
XX and research reagents. AAZ47769 represents the human CD40 nucleotide
XX sequence. AAZ47770 to AAZ47772 represent human CD40 forward and reverse
XX PCR primers, and a human CD40 PCR probe, respectively. AAZ47773 to
XX AAZ47775 represent other PCR primers and a probe used in the

CC exemplification of the present invention

XX Sequence 23 BP; 1 A; 5 C; 8 G; 9 T; 0 U; 0 Other;

SQ Query Match 2.3%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GAACAGAGAGACACACTGCCACC 282
DB 23 GAACAGAGAGACACACTGCCACC 1

RESULT 42

AAZ47770
ID AAZ47770 standard; DNA; 23 BP.

AC AAZ47770;

DT 02-MAR-2000 (first entry)

DE Human CD40 forward PCR primer SEQ ID NO:86.

KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
expression; immune disease; inflammatory disease; immunomodulatory;
anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;
hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
inflammatory bowel disease; asthma; psoriasis; cancer; tumour;
PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

PN WO957320-A1.

PD 11-NOV-1999.

PF 22-APR-1999; 99WO-US008765.

PR 01-MAY-1998; 98US-00071433.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CP, Cowser LM;

XX WPI, 2000-062158/05.

DR Antisense molecules directed against nucleic acid encoding human CD40,
for treating e.g. immune, inflammatory or hyperproliferative diseases.

XX Example 13; Page 50; 102pp; English.

PS AAZ47685 to AAZ47768 represent phosphorothioate antisense
XX oligonucleotides targeted to human CD40, which can be used to inhibit the
XX expression of human CD40. CD40 is involved in lymphocyte activation,
XX tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
XX prevent immune-associated diseases (specifically guest vs. host disease,
XX allograft rejection or autoimmune diseases); inflammation (specifically
XX asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
XX disease or psoriasis) or hyperproliferation (specifically cancer and
XX tumours). the antisense oligonucleotides are also useful as diagnostic
XX and research reagents. AAZ47769 represents the human CD40 nucleotide
XX sequence. AAZ47770 to AAZ47772 represent human CD40 forward and reverse
XX PCR primers, and a human CD40 PCR probe, respectively. AAZ47773 to
XX AAZ47775 represent other PCR primers and a probe used in the
XX exemplification of the present invention

SQ Sequence 23 BP; 8 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAACGGAATGC 224
DB 1 CAGAGTTCACTGAACGGAATGC 23

RESULT 43

ACH66633
ID ACH66633 standard; DNA; 23 BP.

XX AC ACH66633;

XX DT 06-NOV-2003 (first entry)

XX DE Real-time PCR probe used to detect human CD40 expression.

KW Human; ss; PCR; probe; real-time PCR; costimulatory molecule; CD40;
major histocompatibility complex; MHC; class I; class II; antigen;
tumour; deacetylase inhibitor; DAI; tumourgenesis; immune system;
T lymphocyte; T cell activation; immunogenicity; antigen presentation;
cell lysis; trichostatin A; TSA; sodium butyrate; cytostatic; CD40.

OS Homo sapiens.

OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= 5' terminal 6-carboxyfluorescein (FAM) "

FT modified_base 23

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= 3' terminal N,N,N'-tetramethyl-6-

FT carboxyrhodamine (TAMRA) "

XX US6518012-B1.

XX PD 11-FEB-2003.

XX PF 31-MAR-2000; 2000US-00540257.

XX PR 02-APR-1999; 99US-0127591P.

XX PR 29-JUL-1999; 99US-0146275P.

XX PA (HEAL-) HEALTH RES INC.

XX PI Tomasi TB;

XX DR WPI, 2003-575859/54.

XX Increasing expression of gene in tumor cells in vitro comprises
contacting tumor cells with deacetylase inhibitor.

XX Example 1; Fig 9; 20pp; English.

XX The invention discloses a method for increasing the expression of
costimulatory molecules, such as CD40, and major histocompatibility
complex (MHC) class I and class II antigens in tumour cells in vitro. The
method comprises contacting the tumour cells with deacetylase inhibitor
(DAI). Tumourgenesis is related, in part, to the failure of the immune
system to reject spontaneously arising tumours by responding
appropriately to tumour antigens. Induction of T lymphocytes is
considered to be a critical initial step and T cell activation requires
an antigen specific signal, which involves the antigenic peptide and the
MHC class I and II proteins. The increased expression of these molecules
increases the immunogenicity of tumours and their susceptibility to
lysis. The inhibitors of deacetylation, at low concentrations, produce
little or no apoptosis and maintain a normal cell cycle. The expression
of MHC genes, and other molecules of immunologic importance, in antigen
presentation and cell lysis on cells is induced. The DAIs are preferably
trichostatin A (TSA) or sodium butyrate. The sequence presented is a real
-time PCR probe used to detect expression levels of the human CD40 gene

```
XX SQ Sequence 23 BP; 1 A; 8 C; 7 G; 7 T; 0 U; 0 Other;
Query Match      2.3%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 58 TGCCTCTGCACTGGCTCTCTGG 80
Db 1 TGCCTCTGCACTGGCTCTCTGG 23

RESULT 44
ADY75648/C
ID ADY75648 standard; DNA; 23 BP.
XX
AC ADY75648;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human CD40 reverse RT-PCR primer.
XX
KW RT-PCR; primer; ss; diagnosis; drug discovery; mass spectroscopy;
KW reverse transcriptase PCR; CD40.
XX
OS Homo sapiens.
XX
PN WO2005023986-A2.
XX
PD 17-MAR-2005.
XX
PF 07-SEP-2004; 2004WO-US028879.
XX
PR 04-SEP-2003; 2003US-0500723P.
PR 04-SEP-2003; 2003US-0500724P.
PR 04-SEP-2003; 2003US-0500730P.
PR 04-SEP-2003; 2003US-0500732P.
PR 11-SEP-2003; 2003US-0500824P.
PR 11-SEP-2003; 2003US-0502007P.
PR 17-SEP-2003; 2003US-0502076P.
PR 17-SEP-2003; 2003US-0504495P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freier SM;
XX
XX WPI; 2005-233282/24.
XX
XX Selecting a target molecule having affinity for a ligand that is equal
XX to/greater than a baseline affinity by introducing a target molecule into
XX a ligand and standard target test mixture and identifying complex by mass
XX spectrometer.
XX
XX Example 65; SEQ ID NO 153; 314pp; English.
XX
XX The invention relates to selecting a target molecule that has an affinity
XX for a ligand that is equal to or greater than a baseline affinity, ligand
XX comprises introducing a target molecule into a test mixture of the ligand
XX and a standard target, introducing the test mixture into a mass
XX spectrometer and identifying any complexes of the target molecule and the
XX ligand. Also included are a method of detecting a ligand-target complex
XX having an affinity as expressed as a dissociation constant of nanomolar-
XX 100 millimolar, a method for determining the relative interaction between
XX at least two molecules determining target a ligand, a method of
XX determining binding interaction (between a first target molecule and a
XX second target molecule with respect to a ligand), a method of determining
XX the relative proximity of binding sites for a first target molecule and a
XX second target molecule on a ligand, a method of determining the relative
XX orientation of a first target molecule to a second target molecule when
XX bound to a ligand, a method for screening target molecules having binding
XX affinity to a ligand, a method for modulating the binding affinity of a
XX target molecule for a ligand, a method for refining the binding of a
XX target molecule to a ligand, a method of favoring an alternate structure
```

```
CC of an oligomer, a method for identifying a ligand that alters a target
CC compound secondary structure, a method of determining the relative change
CC in proximity of binding sites for a first ligand and a second ligand on a
CC target substrate influenced by the first ligand, a method of determining
CC the relative change in proximity of a first binding site for a binding
CC ligand and a second binding site for a second binding ligand on a target,
CC a method of determining the relative orientation of a first ligand to a
CC second ligand when bound to a target substrate, an oligomeric compound
CC comprising a nucleotide sequence at least 80% complementary to a target
CC RNA (where the oligomeric compound comprises 21-24 nucleotides, and
CC comprises a nucleotide sequence that corresponds to a portion of the
CC nucleotide sequence of a larger oligomeric compound that comprises a
CC stemloop structure), a method of modulating transcription in a cell, a
CC method of modulating translation in a cell, a method of modulating a
CC conversion of a precursor RNA into a microRNA in a cell, a method of
CC generating a set of (oligomeric) compounds that modulate the expression
CC of a target nucleic acid molecule, a computer formatted medium comprising
CC computer readable instructions for identifying active compounds or for
CC performing the method above, a method of predicting evolutionarily
CC allowed mutations of a microRNA, a method of grouping biological members
CC according to a grouping criteria, a method of determining a blur-factor
CC and a method of determining a group of probable mutations for a microRNA.
CC The methods of the invention may be applied to the design of siRNA (short
CC interfering RNA) and antisense oligonucleotides. The method is useful for
CC determining the mode of binding interaction between two or more target
CC molecules to the ligand as well as their relative affinities. The
CC oligomeric compounds are useful in drug discovery and target validation,
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence is an RT-PCR (reverse transcriptase PCR) primer for
CC human CD40 mRNA used to assess expression of CD40 during treatment with
CC antisense oligonucleotides targeted to the human CD40 gene, designed
CC according to the methods of the invention.
XX
```

SQ Sequence 23 BP; 1 A; 5 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 14; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GAACAGAGAGACACACTGCCACC 282

Db 23 GAACAGAGAGACACACTGCCACC 1

RESULT 45

ADY75647

ID ADY75647 standard; DNA; 23 BP.

XX AC ADY75647;

XX XX

DT 02-JUN-2005 (first entry)

XX XX

DE Human CD40 forward RT-PCR primer.

XX XX

KW RT-PCR; primer; ss; diagnosis; drug discovery; mass spectroscopy;

KW reverse transcriptase PCR; CD40.

XX XX

OS Homo sapiens.

XX XX

PN WO2005023986-A2.

XX XX

PD 17-MAR-2005.

XX XX

PF 07-SEP-2004; 2004WO-US028879.

XX XX

PR 04-SEP-2003; 2003US-0500723P.

PR 04-SEP-2003; 2003US-0500724P.

PR 04-SEP-2003; 2003US-0500730P.

PR 04-SEP-2003; 2003US-0500732P.

PR 11-SEP-2003; 2003US-0500824P.

PR 11-SEP-2003; 2003US-0502007P.

PR 17-SEP-2003; 2003US-0502076P.

PR 17-SEP-2003; 2003US-0504495P.

XX PA (ISIS-) ISIS PHARM INC.
XX PI Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freier SM;
XX DR WPI; 2005-233282/24.
XX PT Selecting a target molecule having affinity for a ligand that is equal
XX PT to/greater than a baseline affinity by introducing a target molecule into
XX PT a ligand and standard target test mixture and identifying complex by mass
XX PT spectrometer.
XX PS
XX PS Example 65; SEQ ID NO 152; 314pp; English.
XX PS
XX CC The invention relates to selecting a target molecule that has an affinity
XX CC for a ligand that is equal to or greater than a baseline affinity,
XX CC comprises introducing a target molecule into a test mixture of the ligand
XX CC and a standard target, introducing the test mixture into a mass
XX CC spectrometer and identifying any complexes of the target molecule and the
XX CC ligand. Also included are a method of detecting a ligand-target complex
XX CC having an affinity as expressed as a dissociation constant of nanomolar-
XX CC 100 millimolar, a method for determining the relative interaction between
XX CC at least two molecules determining target a ligand, a method of
XX CC determining binding interaction (between a first target molecule and a
XX CC second target molecule with respect to a ligand), a method of determining
XX CC the relative proximity of binding sites for a first target molecule and a
XX CC second target molecule on a ligand, a method of determining the relative
XX CC orientation of a first target molecule to a second target molecule when
XX CC bound to a ligand, a method for screening target molecules having binding
XX CC affinity to a ligand, a method for modulating the binding affinity of a
XX CC target molecule for a ligand, a method for refining the binding of a
XX CC target molecule to a ligand, a method of favoring an alternate structure
XX CC of an oligomer, a method for identifying a ligand that alters a target
XX CC compound secondary structure, a method of determining the relative change
XX CC in proximity of binding sites for a first ligand and a second ligand on a
XX CC target substrate influenced by the first ligand, a method of determining
XX CC the relative change in proximity of a first binding site for a binding
XX CC ligand and a second binding site for a second binding ligand on a target,
XX CC a method of determining the relative orientation of a first ligand to a
XX CC second ligand when bound to a target substrate, an oligomeric compound
XX CC comprising a nucleotide sequence at least 80% complementary to a target
XX CC RNA (where the oligomeric compound comprises 21-24 nucleotides, and
XX CC comprises a nucleotide sequence that corresponds to a portion of the
XX CC nucleotide sequence of a larger oligomeric compound that comprises a
XX CC stemloop structure), a method of modulating transcription in a cell, a
XX CC method of modulating translation in a cell, a method of modulating a
XX CC conversion of a precursor RNA into a microRNA in a cell, a method of
XX CC generating a set of (oligomeric) compounds that modulate the expression
XX CC of a target nucleic acid molecule, a computer formatted medium comprising
XX CC computer readable instructions for identifying active compounds or for
XX CC performing the method above, a method of predicting evolutionarily
XX CC allowed mutations of a microRNA, a method of grouping biological members
XX CC according to a grouping criteria, a method of determining a blur-factor
XX CC and a method of determining a group of probable mutations for a microRNA.
XX CC The methods of the invention may be applied to the design of siRNA (short
XX CC interfering RNA) and antisense oligonucleotides. The method is useful for
XX CC determining the mode of binding interaction between two or more target
XX CC molecules to the ligand as well as their relative affinities. The
XX CC oligomeric compounds are useful in drug discovery and target validation,
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
XX CC The present sequence is an RT-PCR (reverse transcriptase PCR) primer for
XX CC human CD40 mRNA used to assess expression of CD40 during treatment with
XX CC antisense oligonucleotides targeted to the human CD40 gene, designed
XX CC according to the methods of the invention.
XX CC
XX CC Sequence 23 BP; 8 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX CC
XX CC Query Match 2.3%; Score 23; DB 14; Length 23;
XX CC Best Local Similarity 100.0%; Pred. No. 1.5e+04;
XX CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC 202 CAGAGTTCACTGAAACGGAATGC 224
XX CC |||||||||||||||||||||

Db 1 CAGAGTTCACTGAAACGGAATGC 23

Search completed: February 5, 2006, 09:45:54
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6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gss1:
10: gb_gss2:
11: gb_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.0	50	1	AU107930
2	48.4	4.8	50	1	AU107931
3	46.4	4.6	49	8	H94398
4	40	4.0	50	1	AU107932
5	38.8	3.9	48	8	H95733
6	22.8	2.3	34	1	A1431428
7	21.8	2.2	49	10	CG732711
8	21	2.1	50	1	AU106947
9	20.6	2.1	43	1	A1440496
10	20.6	2.1	46	1	A1250491
11	20.6	2.1	46	1	A1582504
12	20.6	2.1	50	1	AU106810
13	20.4	2.0	40	1	A1678633
14	20.4	2.0	46	10	C2265995
15	20.4	2.0	48	1	C2265995
16	20.2	2.0	49	9	BA399365
17	20.2	2.0	50	1	AU107938
18	20	2.0	45	2	BE393504
19	19.8	2.0	50	1	AU102718
20	19.8	2.0	50	1	AU104759
21	19.8	2.0	50	1	AU104763
22	19.6	2.0	41	9	A2449036

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c 96 18.2 1.8 47 9 AZ805275 2M0066P01
c 97 18.2 1.8 48 9 AZ993115 2M0278G04
c 98 18.2 1.8 49 1 AI001175 ov19a12.8
c 99 18.2 1.8 49 1 AA122130 zn82f09.r
c 100 18.2 1.8 50 1 AA798983 vv95f06.f
c 101 18.2 1.8 50 1 AI010452 AU102452
c 102 18.2 1.8 50 1 AU104124 AU104124
c 103 18.2 1.8 50 1 AU104940 AU104940
c 104 18.2 1.8 50 1 AU104943 AU104943
c 105 18.2 1.8 50 1 AU105236 AU105236
c 106 18.2 1.8 50 1 AU106428 AU106428
c 107 18.2 1.8 50 1 AU106860 AU106860
c 108 18.2 1.8 50 1 AU107339 AU107339
c 109 18.2 1.8 50 6 CB410572 NISC nc12
c 110 18 1.8 29 8 DN955450 it97h12.g
c 111 18 1.8 42 9 CC326042 RS7753.Ba
c 112 18 1.8 43 10 CZ477690 dl1365-3p
c 113 18 1.8 45 5 BX621624 BX621624
c 114 18 1.8 46 3 BI488502 603021011
c 115 18 1.8 48 1 AV845590 AV845590
c 116 18 1.8 48 6 CA965843 CCLX05a19
c 117 18 1.8 49 1 AA934654 co01e06.8
c 118 18 1.8 49 9 CC887819 SALK 1508
c 119 18 1.8 50 1 AU102653 AU102653
c 120 18 1.8 50 1 AU103142 AU103142
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ALIGNMENTS

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RESULT 1
AU107930 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU107930 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC00913, mRNA sequence.
ACCESSION AU107930.1 GI:13557452
VERSION AU107930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
TITLE ENBO Rep. 2 (5), 388-393 (2001)
JOURNAL 11375929
PUBMED Contact: Yutaka Suzuki
COMMENT Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN
Query Match 5.0%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 18 AGTGGTCTCGCGCTGGTCTTACCTGCCATGGTTCCTGCTGCTGCTGCA 67
|||||
Db 1 AGTGGTCTCGCGCTGGTCTTACCTGCCATGGTTCCTGCTGCTGCTGCA 50
|||||

RESULT 2
AU107931 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU107931 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC02683, mRNA sequence.
ACCESSION AU107931.1 GI:13557453
VERSION AU107931
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
TITLE ENBO Rep. 2 (5), 388-393 (2001)
JOURNAL 11375929
PUBMED Contact: Yutaka Suzuki
COMMENT Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

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Query Match 4.8%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.044;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 23 TCCTGCCGCTGGTCTCACCTGCCATGGTTCGCTGCTGCTGCGTGGC 72
|||||
Db 1 TCCTGCCGCTGGTCTCACCTGCCATGGTTCGCTGCTGCTGCGTGGC 50
|||||

RESULT 3
H94398 49 bp mRNA linear EST 25-NOV-1996
LOCUS H94398 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION IMAGE:243016 5' similar to gb:X80592 CD40L RECEPTOR PRECURSOR
(HUMAN); contains 11 repetitive element ;, mRNA sequence.
ACCESSION H94398
VERSION H94398.1 GI:1102031
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
```



```

REFERENCE
AUTHORS   Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura.Y., Suyama,A. and Sugano,S.
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
PUBMED    11375929
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuki@ims.u-tokyo.ac.jp
          Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES
source    Location/Qualifiers
          1..50
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="ZRV6C565"
          /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      2.1%; Score 21; DB 1; Length 50;
Best Local Similarity 73.0%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY  781 CCAACACGTGCTCCTCAGTGGAGGAGACTTTACATGG 817
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  50 CCAACGCTGCTGCCACAGACCGAGAGGCTTAAATGG 14

RESULT 9
AI440496
LOCUS    tc98hh2.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2073287 3,
DEFINITION similar to TR:Q04118 SALIVARY PROLINE-RICH GLYCOPROTEIN G1
          PRECURSOR. ; contains MER22.t1 MSRI repetitive element ;, mRNA
          sequence.
ACCESSION AI440496
VERSION   AI440496.1 GI:4300635
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 43)
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
          M.D., Louis M. Staudt, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Trace considered overall poor quality
          Insert Length: 505 Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence stop: 1.
          Location/Qualifiers
          1..43
          /organism="Homo sapiens"

FEATURES
source    Location/Qualifiers
          1..43
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="ZRV6C565"
          /clone_lib="Sugano Homo sapiens cDNA library"
          /dev_stage="adult"
          /sex="female"
          /tissue_type="borderline ovarian carcinoma"
          /lab_host="DH10B"
          /clone_lib="NCI CGAP Ov34"
          /note="Organ: ovary; Vector: pAMP1; mRNA made from
          borderline ovarian carcinoma, cDNA made by oligo-dT
          priming. Directionally cloned. Size-selected on agarose
          gel, average insert size 500 bp. Primary library,
          non-amplified."

```

```

ORIGIN
Query Match      2.1%; Score 20.6; DB 1; Length 43;
Best Local Similarity 74.3%; Pred. No. 1.9e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY  707 GAAGCCCAACCAATAAGCCGCCACCCCAAGCAGG 741
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  8 GAAAAAAGAAAAAGAGGCCCCCCCCCCCCCAAGGGG 42

RESULT 10
AI250491/c
LOCUS    qx27h02.x1 NCI CGAP Ov34 Homo sapiens cDNA clone IMAGE:2002611 3,
DEFINITION similar to gb:L21696 cds1 PROTHYMOSIN ALPHA (HUMAN); contains
          element MER25 repetitive element ;, mRNA sequence.
ACCESSION AI250491
VERSION   AI250491.1 GI:3847020
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 46)
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          unknown library type
          Trace considered overall poor quality
          Insert Length: 404 Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence stop: 1.
          Location/Qualifiers
          1..46
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="IMAGE:2002611"
          /sex="female"
          /tissue_type="borderline ovarian carcinoma"
          /dev_stage="adult"
          /lab_host="DH10B"
          /clone_lib="NCI CGAP Ov34"
          /note="Organ: ovary; Vector: pAMP1; mRNA made from
          borderline ovarian carcinoma, cDNA made by oligo-dT
          priming. Directionally cloned. Size-selected on agarose
          gel, average insert size 500 bp. Primary library,
          non-amplified."

```



```

source
1. 40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2257799"
/tissue_type="poorly differentiated adenocarcinoma with
signal ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/notes="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 2.0%; Score 20.4; DB 1; Length 40;
Best Local Similarity 71.1%; Pred. No. 2.1e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 698 GGTGCCCAAGACCAACATAAGGCCGCCGCCACCCCA 735
||||| ||||| ||||| ||||| ||||| |||||
Db 3 GGGGGGAAGAAAAAACCACCAAAACCCGCCGCCCA 40

RESULT 14
C2265995/c
LOCUS
DEFINITION
C2265995
VERSION
C2265995.1 GI:60393817
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 46)
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1373 Std Error: 0.00
Seg primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="GDB:5937717"
/db_xref="taxon:9606"
/clone="IMAGE:2257799"
/sex="Male"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor N8HOT"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

ORIGIN
Query Match 2.0%; Score 20.4; DB 1; Length 48;
Best Local Similarity 71.1%; Pred. No. 2.2e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 938 CCTGGTGCTGCTGCTGAGGGGTGTCAGGAGAGCGGG 975
||||| ||||| ||||| ||||| ||||| |||||
Db 41 CCTGGTCTGAGAGTCTGCTGCGGGCGGGAGCTGCTG 4

RESULT 16
BH759224/c
LOCUS
DEFINITION
BH759224
49 bp DNA linear GSS 12-MAR-2002
KG00450-3prime Drosophila melanogaster p{SUPor-p} P element
insertion lines Drosophila melanogaster genomic sequence recovered
from 3' end of P element, genomic survey sequence.

LOCUS
AA399365 48 bp mRNA linear EST 08-AUG-1997
zts0d07.s1 Soares ovary tumor N8HOT Homo sapiens cDNA clone
IMAGE:725773 3' similar to WP:CS4G4.1 CE05507 RIBOSOMAL S6 KINASE
; mRNA sequence.
ACCESSION
AA399365
VERSION
AA399365.1 GI:2053171
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 48)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1373 Std Error: 0.00
Seg primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..48
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5937717"
/db_xref="taxon:9606"
/clone="IMAGE:725773"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor N8HOT"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

ORIGIN
Query Match 2.0%; Score 20.4; DB 1; Length 48;
Best Local Similarity 71.1%; Pred. No. 2.2e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 938 CCTGGTGCTGCTGCTGAGGGGTGTCAGGAGAGCGGG 975
||||| ||||| ||||| ||||| ||||| |||||
Db 41 CCTGGTCTGAGAGTCTGCTGCGGGCGGGAGCTGCTG 4

RESULT 16
BH759224/c
LOCUS
DEFINITION
BH759224
49 bp DNA linear GSS 12-MAR-2002
KG00450-3prime Drosophila melanogaster p{SUPor-p} P element
insertion lines Drosophila melanogaster genomic sequence recovered
from 3' end of P element, genomic survey sequence.

```

```
ACCESSION BH759224
VERSION BH759224.1 GI:19352463
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 49)
Levis,R., Hoskins,R., Liao,G., Mozden,N., Tsang,G., He,Y.,
Karpén,G., Bellen,H., Rubin,G. and Spradling,A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
CONTACT: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5108433947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 1 in the 49 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
FEATURES             source
    source            Location/Qualifiers
        1..49
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone_lib="Drosophila melanogaster P{SUPor-P} P element
        insertion lines"
        /note="Inverse PCR was performed on Drosophila
        melanogaster strains each of which contains one or more
        P{SUPor-P} P-element transposon insertion. The resultant
        fragment for each strain was directly sequenced to
        determine the genomic sequence at the site of insertion.
        Details of the protocols used can be found at
        http://www.fruitfly.org/about/methods/inverse.pcr.html."
ORIGIN
Query Match          2.0%; Score 20.2; DB 9; Length 49;
Best Local Similarity 75.8%; Pred. No. 2.5e+06;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 767 CGATCTTCCTGGCTCCACACTGCTGCTCCAGT 799
Db 43 CGCTCTTTGGGGCTCCCAACCCGCTGCTCCATT 11

RESULT 17
AUI07338
LOCUS AUI07338 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS04142, mRNA sequence.
ACCESSION AUI07338
VERSION AUI07338.1 GI:13556859
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
    source            Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CAS04142"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match          2.0%; Score 20.2; DB 1; Length 50;
Best Local Similarity 68.3%; Pred. No. 2.5e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 758 TTTTCCGACGATCTTCCTGGCTCCACACTGCTGCTCCAG 798
Db 3 TATCTCGATGCGCTTCTCTGGCAGCTACATCTGCTCTCG 43

RESULT 18
BE393504
LOCUS BE393504 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3632638 5',
DEFINITION mRNA sequence.
ACCESSION BE393504
VERSION BE393504.1 GI:9338869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 45)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM324 row: e column: 23
High quality sequence stop: 45.
FEATURES             source
    source            Location/Qualifiers
        1..45
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:3632638"
        /tissue_type="endometrium, adenocarcinoma cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC 44"
        /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5',
        adaptor: GGACGAG(G). Library constructed by Ling Hong
        in the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
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Best Local Similarity 72.2%; Pred. No. 2.8e+06; Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 170 CCAGCAGGACAGAACTGGTGCAGTCTGACGACAGCA 205
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Db 4 CCAGCAAGCAGCAGCAGCAGTTCAGCCAGTTCACAGA 39

RESULT 19
AUI02718/c
LOCUS AUI02718.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI02718 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT06130, mRNA sequence.
ACCESSION AUI02718
VERSION AUI02718.1 GI:13552239
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS10241"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 77.4%; Pred. No. 3.2e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 879 TGAGGCTGCACCCACCCAGGAGTGTGGCCAC 909
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 31 TGAGGCTGCAGCCCTCTGGGGTGTAGGGCCAC 1

RESULT 21
AUI04763/c
LOCUS AUI04763.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HST01164, mRNA sequence.
ACCESSION AUI04763
VERSION AUI04763.1 GI:13554284
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT06130"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 63.8%; Pred. No. 3.2e+06; Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 305 CCTAGGCTTCGGGTCAGCAGAGCGCACCTTCAGAAACAGACCA 351
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Db 48 CCCATGGCAGCGGTCAGATTCACAGCGCGGCCGAGAGAGGAACA 2

RESULT 20
AUI04759/c
LOCUS AUI04759.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04759 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS10241, mRNA sequence.
ACCESSION AUI04759
VERSION AUI04759.1 GI:13554280
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS10241"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 77.4%; Pred. No. 3.2e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 879 TGAGGCTGCACCCACCCAGGAGTGTGGCCAC 909
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 31 TGAGGCTGCAGCCCTCTGGGGTGTAGGGCCAC 1

RESULT 21
AUI04763/c
LOCUS AUI04763.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HST01164, mRNA sequence.
ACCESSION AUI04763
VERSION AUI04763.1 GI:13554284
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HST01164"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 77.4%; Pred. No. 3.2e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      879  TGAGGCTGACCCACCCAGGAGTGTGGCCAC 909
      |||||
Db      31  TGAGGCTGACGCGCTCTGGGGTGGAGGCAC 1

RESULT 22
A2449036/c
LOCUS   A2449036           41 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION
clone UUGC1M0247P02 F, genomic survey sequence.
ACCESSION
A2449036
VERSION
A2449036.1 GI:10602425
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0247 row: P column: 02
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 41.

FEATURES
Location/Qualifiers
1..41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0247P02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      2.0%; Score 19.6; DB 9; Length 41;
Best Local Similarity 73.5%; Pred. No. 3.5e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      398  GAGCTGTGTCCTGCACCGCTCATGCTGCCCGCGCTTTGGGGT 439
      |||||
Db      1  GCAGTCGCGCTGCGCCCTCTCTCCGCGCGCTCCCGGGT 42

RESULT 24
AUI04419/c
LOCUS   AUI04419          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION
AUI04419 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP22703, mRNA sequence.
ACCESSION
AUI04419
VERSION
AUI04419.1 GI:13553940
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COLF1717"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      2.0%; Score 19.6; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.7e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      711  CCAACCAATAGGCCCCCAACCCCAAGCAGGAC 744
      |||||
Db      37  CTAGCCCATGAGCCTCACCCCTCAAGCAGGAC 4

RESULT 23
AUI03053
LOCUS   AUI03053          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION
AUI03053 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLF1717, mRNA sequence.
ACCESSION
AUI03053
VERSION
AUI03053.1 GI:13552574
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COLF1717"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      2.0%; Score 19.6; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.7e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      398  GAGCTGTGTCCTGCACCGCTCATGCTGCCCGCGCTTTGGGGT 439
      |||||
Db      1  GCAGTCGCGCTGCGCCCTCTCTCCGCGCGCTCCCGGGT 42

RESULT 24
AUI04419/c
LOCUS   AUI04419          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION
AUI04419 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP22703, mRNA sequence.
ACCESSION
AUI04419
VERSION
AUI04419.1 GI:13553940
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COLF1717"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      2.0%; Score 19.6; DB 9; Length 41;
Best Local Similarity 73.5%; Pred. No. 3.5e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```

JOURNAL
PUBMED
COMMENT

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP22703"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.6; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.7e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 880 GAGGTGCACCCACCCAGGTGGCCACGTGGGCAACAG 921
|||||
Db 46 GAGGCCGCGTATCCAGGATGGCGACGAGTGCACCAACAG 5
|||||

RESULT 25
AZ859427
LOCUS
DEFINITION
2M0165106F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0165106 F, genomic survey sequence.

ACCESSION
AZ859427
VERSION
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: 1 column: 06
Seq primer: CGTTGTAACAGCAGGCCAGT
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0165106"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

Qy 939 CTGGTGTCTGCTGCTGCAGGGGTGCAGCAGAGCGGG 975
|||||
Db 6 CTGGGAGTGGAGGGCTGGGGTGGGGGAGAGCGGG 42
|||||

RESULT 26
CC178199
LOCUS
DEFINITION
XC750 BayGenomics Gene Trap Library pGTLxf Mus musculus CDNA, mRNA
sequence.

ACCESSION
CC178199
VERSION
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 45)
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XC750

FEATURES
source
1..45
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTLxf"
/note="Vector: pGTLxf"

ORIGIN
Query Match 1.9%; Score 19.4; DB 9; Length 45;
Best Local Similarity 64.4%; Pred. No. 4e+06;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."


```

POLYA=No.
FEATURES
    source            Location/Qualifiers
    1..49
        /organism="Litopenaeus vannamei"
        /mol_type="mRNA"
        /db_xref="taxon:6689"
        /cell_type="Hemocyte"
        /dev_stage="adult"
        /clone_lib="Shrimp GS-Vibrio alginolyticus Library"
        /note="Vector: Topo PCR 2.1"
ORIGIN
Query Match      1.9%; Score 19.2; DB 7; Length 49;
Best Local Similarity 64.3%; Pred. No. 4.7e+06;
Matches 27; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Qy 47 CATGGTTCGTCGCTCGACGTGCGTCCTCTGGGGCTGCTT 88
Db 2 CAAGGTTCTTGGGCTCCGTGGTGGTGGTCAGGCGCGGTT 43

RESULT 32
CK734037/c
LOCUS
DEFINITION      CK734037          49 bp mRNA linear EST 17-FEB-2004
                  clone TgSTzyk47h09.y1 TGRH Tachyzoite FL cDNA Toxoplasma gondii CDNA
ACCESSION      CK734037
VERSION        CK734037.1 GI:42587551
KEYWORDS       EST.
SOURCE         Toxoplasma gondii
ORGANISM       Toxoplasma gondii
                Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                Sarcocystidae; Toxoplasma.
REFERENCE
AUTHORS        Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
                Clifton,S., Pape,D., Martin,D., Wylie,T., Dante,M., Marra,M.,
                Hallier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
                Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
                Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
                Toxoplasma EST Project
                Unpublished (2001)
                Contact: Clifton, S.
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: toxo@watson.wustl.edu
                Contact David Sibley (toxost@borcim.wustl.edu) for further
                information relating to organism, libraries, or clone availability.
                Putative full length read
                vector to vector length is
                Seq primer: T7 from Gibco.
FEATURES
    source            Location/Qualifiers
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        /db_xref="taxon:5811"
        /clones="TgSTzyk47h09.y1"
        /dev_stage="Tachyzoite"
        /lab_host="GC10"
        /clone_lib="TGRH Tachyzoite FL cDNA"
        /note="Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; The
                cDNA library was constructed by Keliang Tang, adn Robert
                Cole at Washington University. Total RNA was converted to
                cDNA using the template-switching PCR method (Creator
                SMART cDNA, Clontech, Inc.). First strand was reverse
                transcribed using the CDS III/3' primer and a 5' template
                switch primer using the same primer set and the fragments
                were digested with Sfil. The directional Sfil sites, and
                electroporated into GC10 Competent cells. Antibiotic:
                Chloramphenicol (30ug/ml)"
ORIGIN

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Query Match      1.9%; Score 19.2; DB 7; Length 49;
Best Local Similarity 75.0%; Pred. No. 4.7e+06;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 596 TGTGTCTGTGGTCCCGAGGATCGGTGAGAG 627
Db 49 TGTGTTTGTGTCGACAGATCAGCTGAGAG 18

RESULT 33
AUI02702/c
LOCUS
DEFINITION      AUI02702 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
                  CAS08541, mRNA sequence.
ACCESSION      AUI02702
VERSION        AUI02702.1 GI:13552223
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE
AUTHORS        Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
                  Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
                  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
                  Diverse transcriptional initiation revealed by a fine, large-scale
                  mapping of mRNA start sites
                  ENBO Rep. 2 (5), 388-393 (2001)
                  11375929
COMMENT        Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: yusuzuki@ims.u-tokyo.ac.jp
                Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                Sugano,S. Construction and characterization of a full
                length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                149-156 (1997).
FEATURES
    source            Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CAS08541"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      1.9%; Score 19.2; DB 1; Length 50;
Best Local Similarity 67.5%; Pred. No. 4.7e+06;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 965 GCAGAGCGGGAGCTATGCCAGTCAGTCGCGCCGCTC 1004
Db 45 GCAGTAGCGGTACCGGTACCCCTTTCAGGCCCGAGTTCCTC 6

RESULT 34
AZ369352/c
LOCUS
DEFINITION      AZ369352          39 bp DNA linear GSS 02-OCT-2000
                  LM0119H19R Mouse 10kb plasmid UUGCJM library Mus musculus genomic
                  clone UUGCJM0119H19 R, genomic survey sequence.
ACCESSION      AZ369352
VERSION        AZ369352.1 GI:10483052
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidae; Muridae; Murinae; Mus.
                1 (bases 1 to 39)
                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

```

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0119 row: H column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 39.

FEATURES source

1. .39
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0119H19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.9%; Score 19; DB 9; Length 39;
 Best Local Similarity 81.5%; Pred. No. 5e+06;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 970 AGCGGGAGCTATGCCAGTCAGTGCC 996
 |||||
 Db 32 AGAGTGGATTATGCCAGTCGTGCCC 6

RESULT 35
 AG218322
 LOCUS 48 bp DNA linear GSS 03-SEP-2002
 DEFINITION Drosophila melanogaster DNA, clone:NP0527-5-1, flanking P{GAWB} transposon insertion, genomic survey sequence.
 ACCESSION AG218322
 VERSION AG218322.1 GI:22765322
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1

AUTHORS

Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H., Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R., Uemura, T., Yoshihara, M. and Goto, S.
 Location of a collection of Gal4 enhancer traps

TITLE

locations of a collection of Gal4 enhancer traps

JOURNAL

Genesis (2002) In press

AUTHORS

Hayashi, S.

TITLE

Direct Submission

JOURNAL

Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for Developmental Biology, Laboratory for Morphogenetic Signaling; Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan (E-mail: shayashi@db.riken.go.jp, Tel: 81-78-301-3184, Fax: 81-78-301-3183)
 This clone was isolated from genomic DNA flanking an insertion of the P element vector P{GAWB} of a Drosophila strain.

COMMENT

the P element vector P{GAWB} of a Drosophila strain.

FEATURES

Location/Qualifiers
 source

1. 48
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="NP0527"
 /db_xref="taxon:7227"
 /chromosome="3"
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 /clone="NP0527-5-1"
 /note="flanking P{GAWB} transposon insertion"

ORIGIN

Query Match 1.9%; Score 19; DB 10; Length 48;
 Best Local Similarity 71.4%; Pred. No. 5.3e+06;
 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 284 GCACAAATATCGACCCCACTAGGCTTCGGG 318
 |||||
 Db 5 GCGCCAAACTTCGACTGCAACCGGGCATCGCG 39

RESULT 36
 AUI05004

LOCUS 50 bp mRNA linear EST 28-JAN-2004
 DEFINITION AUI05004 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC07808, mRNA sequence.

ACCESSION

AUI05004

VERSION

AUI05004.1 GI:13554525

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929

JOURNAL

PUBMED

COMMENT

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers
 source

FEATURES

Location/Qualifiers
 source

1. 50
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="HRC07808"

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Query Match          1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 5.4e+06;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 941 GGTGCTGCTGCTGCAGGGGTGCAGGCAGAGCGGG 975
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 GGTGGCGTCTGCAGAGTGGCTGATGCAGAGG 45

RESULT 37
AUI06809 Sugano Homo sapiens cDNA library EST 28-JAN-2004
LOCUS CAS03140, mRNA sequence.
DEFINITION AUI06809 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI06809
VERSION AUI06809.1 GI:13556330
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
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/clone="CAS03140"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 934 AGACCTGCTGCTGCTGCTGCAGGGGTGCAGGCAGAGCGGG 976
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AGACCTAGTCCGTGCTGCTGCTGCAGAGGTATCGGCGGGCGACGC 49

RESULT 38
AUI06811 Sugano Homo sapiens cDNA library EST 28-JAN-2004
LOCUS CAS11251, mRNA sequence.
DEFINITION AUI06811 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI06811
VERSION AUI06811.1 GI:13556332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

```

REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
Location/Qualifiers
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ORIGIN
Query Match          1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 934 AGACCTGCTGCTGCTGCTGCAGGGGTGCAGGCAGAGCGGG 976
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Db 7 AGACCTAGTCCGTGCTGCTGCTGCAGAGGTATCGGCGGGCGACGC 49

RESULT 39
AUI06812 Sugano Homo sapiens cDNA library EST 28-JAN-2004
LOCUS HEP23095, mRNA sequence.
DEFINITION AUI06812 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI06812
VERSION AUI06812.1 GI:13556333
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yezuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
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Location/Qualifiers
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

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Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 934 AGAGCTGGTGTCTGCTGCAGGGGTGCAGGCAGAGCGGG 976
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Db 7 AGAGCTAGTGGTGGTGGAGAGGATATCGGACGGGCACGC 49

RESULT 43
AUI06816
LOCUS AUI06816 Sugano Homo sapiens cDNA library EST 28-JAN-2004
DEFINITION HS104301, mRNA sequence.
ACCESSION AUI06816
VERSION AUI06816.1 GI:13556337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 934 AGAGCTGGTGTCTGCTGCAGGGGTGCAGGCAGAGCGGG 976
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AGAGCTAGTGGTGGTGGAGAGGATATCGGACGGGCACGC 49

RESULT 44
AUI06818
LOCUS AUI06818 Sugano Homo sapiens cDNA library EST 28-JAN-2004
DEFINITION HS105825, mRNA sequence.
ACCESSION AUI06818
VERSION AUI06818.1 GI:13556339
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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KEYWORDS EST.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
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Query Match 1.9%; Score 19; DB 1; Length 50;
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Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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